



XX  
 CC This invention describes a novel multivalent Fv-antibody construct with  
 CC at least four variable domains that are connected to one another by 1,  
 CC 2 and 3 peptide linkers. The construct has antiviral, antibacterial  
 CC and cytostatic activity. The multivalent Fv-antibody constructs are  
 useful for the diagnosis and/or therapy of disease, especially viral,  
 bacterial or tumor diseases. The multivalent Fv-antibody constructs have  
 increased stability when in the form of a single chain dimer. This  
 sequence represents a tetravalent Fv antibody construct composed of the  
 CC antibody 9E10 epitope in expression plasmid pDISC3x19 SL  
 XX  
 SQ Sequence 539 AA:

Query	Match	Score	DB	Length
Best Local Similarity	88.2%	21;	539;	
Matches	285;	Pred. No.	3.5e-80;	
	Conservative	2;	Mismatches	4;
		Indels	248;	Gaps 3;
QY	1 MKYLPTAAAGLLLAQAPAMQVOLQSGAELARPGASVMSCKASGYFTTRYMHWK 60			
QY	1 mkyllptaaglllaaqapamaqvlqsgaelarpgasvmsckasgyfttrymhwk 60			
Db	61 QRPQGLEWIGYINPSRGYTYNNQKFRDKATLTIDKSSSTAYMQLSSLSBDSAVYCAR 120			
QY	61 qrpqglewiyqinpsrgytyynqfkdkatlttdksstaymqissltsdavycar 120			
Db	121 YYDDHYSLDYWQGTMLTWSAKTPKL----- 148			
QY	121 yyddhysldywqgtltwsaktpkldgdliltqtpaslavsigratiskasqsvd 180			
Db	121 yyddhysldywqgtltwsaktpkldgdliltqtpaslavsigratiskasqsvd 180			
QY	149 ----- 148			
Db	181 ygdsvlynwqgipgppklliydasnlvsgipprfsgsgqtdftlnihpvekdaaty 240			
QY	149 ----- 148			
Db	241 hcqstedpwtfggtkleikradaaaagggpsqyqlqqsgaelvrpgsvkisckasy 300			
QY	149 ----- EEEFP----- 153			
Db	301 afssywmnwvkqrpqglewigqiwpgdgatnyngfkfkgatltadessstaymqlsla 360			
QY	154 ----- SEARV-----DIVTQSPTMSAS 172			
Db	361 sedsavycarrettvtvgryyandywggtstvtsaktpklgdivitqspains 420			
QY	173 PGEKTTMCASSSYMMNQOKGTSKSPRKWYDTSKALASGVPAHFRGCGSTSLSLT 232			
Db	421 pgekytmtcsasssyymwyqksgstsprkiydtkslasgvphfrgsgsgtyslti 480			
QY	233 SGMEAEDAATYYCQWSSNFTFGGTKELEINRADAPTGSESEQKLITSEEDINSHHHHH 291			
Db	481 sgmeedaataytcyccqwsnptffsgtkleinradaptgseqkliseedlnshhhh 539			
RESULT	2			
ID	AY50822 standard; Protein; 554 AA.			
AC	AY50822;			
XX	18-FEB-2000 (first entry)			
DE	Fv-antibody construct containing antibody 9E10 epitope protein.			
KW	Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic; diagnosis; therapy; disease.			
OS	Synthetic.			
XX	DE19819846-A1.			
PD	11-NOV-1999.			

XX	PF	05-MAY-1998:	98DE-1019846.
CC	XX	05-MAY-1998:	98DE-1019846.
CC	PR	(DEKR-) DEUT KRBSFORSCHUNGSZENTRUM.	
CC	XX	Little M, Kipriyanov S;	
CC	XX	WPI; 2000-024472/03.	
CC	DR	N-PSDB; AA243431.	
XX	PT	Multivalent Fv-antibody constructs with at least four variable domains connected by 1, 2 and 3 peptide linkers	
XX	PT	Example 1; Fig 5; 14PP; German.	
QY	1 MKYLPTAAAGLLLAQAPAMQVOLQSGAELARPGASVMSCKASGYFTTRYMHWK 60		
QY	1 mkyllptaaglllaaqapamaqvlqsgaelarpgasvmsckasgyfttrymhwk 60		
Db	61 QRPQGLEWIGYINPSRGYTYNNQKFRDKATLTIDKSSSTAYMQLSSLSBDSAVYCAR 120		
QY	61 qrpqglewiyqinpsrgytyynqfkdkatlttdksstaymqissltsdavycar 120		
Db	121 YYDDHYSLDYWQGTMLTWSAKTPKL----- 148		
QY	121 yyddhysldywqgtltwsaktpkldgdliltqtpaslavsigratiskasqsvd 180		
Db	121 yyddhysldywqgtltwsaktpkldgdliltqtpaslavsigratiskasqsvd 180		
QY	149 ----- 148		
Db	181 ygdsvlynwqgipgppklliydasnlvsgipprfsgsgqtdftlnihpvekdaaty 240		
QY	149 ----- 148		
Db	241 hcqstedpwtfggtkleikradaaaagggpsqyqlqqsgaelvrpgsvkisckasy 300		
QY	149 ----- EEEFP----- 153		
Db	301 afssywmnwvkqrpqglewigqiwpgdgatnyngfkfkgatltadessstaymqlsla 360		
QY	154 ----- SEARV-----DIVTQSPTMSAS 172		
Db	361 sedsavycarrettvtvgryyandywggtstvtsaktpklgdivitqspains 420		
QY	173 PGEKTTMCASSSYMMNQOKGTSKSPRKWYDTSKALASGVPAHFRGCGSTSLSLT 232		
Db	421 pgekytmtcsasssyymwyqksgstsprkiydtkslasgvphfrgsgsgtyslti 480		
QY	233 SGMEAEDAATYYCQWSSNFTFGGTKELEINRADAPTGSESEQKLITSEEDINSHHHHH 291		
Db	481 sgmeedaataytcyccqwsnptffsgtkleinradaptgseqkliseedlnshhhh 539		
QY	149 ----- EEEFP----- 153		
Db	301 rpgsvkisckasyafssywmnwvkqrpqglewigqiwpgdgatnyngfkfkgatlt 360		
QY	154 ----- SEARV----- 158		
Db	361 desstaymqisslasedsavyfcarrettvtvgryyandywggtstvtsaktpklg 420		
QY	159 ----- EEEFP----- 158		
Db	421 gdvltqspalmsaspgekvttmtcsasssyymwyqksgstsprkiydtkslasgvpa 480		
QY	218 HFRGCGSTSLSLTSGMMEAATYYCQWSSNFTFGGTKELEINRADAPTGSESEQKL 277		
Db	481 hfrgsgstsylsitsigmeedaataytcyccqwsnptffsgtkleinradaptgseqkl 540		
QY	278 ISEEDINSHHHHH 291		
Db	541 iseedinshhhhhh 554 !		

	RESULT	3
AC	AAW82482	
ID	AAW82482	standard; Protein: 288 AA.
XX	XX	
XX	XX	
AC	AAW82482;	
ID	AAW82316	
XX	XX	
DT	26-FEB-1999	(first entry)
XX	XX	
DE	Mouse bispecific antibody variant OKT3/anti-CD3 protein.	
XX	XX	
KW	OKT3; monoclonal antibody; MAb; point mutation; transplant rejection; organ recipient; diagnosis; tumour; therapy; diabody; anti-CD19; anti-CD3.	
XX	XX	
OS	Mus sp.	
OS	Synthetic.	
XX	XX	
PN	DB19721700-C1.	
XX	XX	
X	19-NOV-1998.	
XX	XX	
PF	23-MAY-1997;	97DE-1021700.
XX	XX	
PR	23-MAY-1997;	97DE-1021700.
XX	XX	
PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.	
XX	XX	
PT	Kipriyanov S, Little M, Moldenhauer G;	
XX	XX	
DR	WPI; 1998-596150/51.	
XX	XX	
PT	Monoclonal antibody OKT3 with point-mutation - where cysteine is replaced by another polar amino acid, useful for controlling transplant rejection, and in tumour diagnostics and therapy	
PT	XX	
PS	Disclosure; Fig 3; 8pp; German.	
XX	XX	
CC	This sequence represents a protein which has anti-CD3 activity and is encoded by a monoclonal antibody (MAb) diabody derived from OKT3 with a point-mutation where Cys at position H100A is replaced with another polar amino acid, in this example Ser. The diabody encodes two OKT3 proteins, one which has anti-CD19 activity and one with anti-CD3 activity. The MAb is used in lowering or eliminating the transplant rejection in an organ recipient and for diagnostic methods for tumours and tumour therapy.	
CC	XX	
CC	Sequence 288 AA:	
SQ		
Query Match	84.7%	Score 1300.5; DB 19; Length 288;
Best Local Similarity	85.3%	Pred. No. 5 2e-77;
Matches	255;	Conservative 10; Mismatches 15; Indels 19; Gaps 3;
OY	1	MKYLPLPAAAGLILLAAQPMAMAOVQLOOGSAGLARCGASVMSCKASGYTFTRYTWWK 60
Db	1	mkylipltaagllilaqpmpanaqvqqlqsgaelvrpgssvkiscasgavfssywinwvkw 60
OY	61	ORPGQGLEWIGYINPSRGTYNQNKDKRATITDSSSTAYMQLSLTSEDAVYCAR 119
Db	61	qrpqgglewiyinpsrgtynqkfkakattdksstaysmqllsitsedsavyycar 120
OY	61	qrpqgglewiyinpsrgtynqkfkakattdksstaysmqllsitsedsavyycar 120
Db	120	-----RYDDHYSYDWGQCTLTIVSSAKTPKLEEGFSEARVDIVLTOPATMSA 172
OY	121	rettttgrgy--yandywgqgtsvtssaktptkigg-----divlcpainsmas 169
Db	170	pgekvutmcassssvsmnwooksgtspkwiydisklasgvpaahergsosgtstlti 229
OY	173	sqmeaedaatyvqcqssnppifgsgtkleinradaptapgeqkliiseedlnshhhh 291
Db	230	sqmeaedaatcycqcsqsnppifqsgtkeinradaptapgeqkliiseedlnshhhh 288
Query Match	78.7%	Score 1208.5; DB 19; Length 288;
Best Local Similarity	78.7%	Pred. No. 4.7e-71;
Matches	233;	Conservative 17; Mismatches 33; Indels 13; Gaps 2;
OY	1	MKYLPLPAAAGLILLAAQPMAMAOVQLOOGSAGLARCGASVMSCKASGYTFTRYTWWK 60
Db	1	mkylipltaagllilaqpmpanaqvqqlqsgaelvrpgssvkiscasgavfssywinwvkw 60
OY	61	ORPGQGLEWIGYINPSRGTYNQNKDKRATITDSSSTAYMQLSLTSEDAVYCAR 120
Db	61	qrpqgglewiyinpsrgtynqkfkakattdksstaysmqllsitsedsavyycar 120
OY	121	YDDHYSYDWGQCTLTIVSSAKTPKLEEGFSEARVDIVLTOPATMSA 172
Db	121	yyddhysydwgqgttivssaktptkigg-----dilqtqbslavlggratis 172
OY	181	CSASSV---SYMMWQOKSGTSPRKWIVOTSKLASGVPAHFRSGSGSYLSITGM 235
Db	173	chassdydgsylnyyqqgpprllydngsqqsfdfthipv 232
OY	236	EADATYVCOOWSNIFTEGGSTKLEINRADAPTAPGEQKLIISEEDLNSHHHH 291
Db	233	ekvdavtchcqstdpwtfggtkleikadaaagseqkiseedlnshhhh 288

	RESULT	5
AAW82317	ID	AAW82317 standard; Protein; 288 AA.
XX	ID	AAW43749 standard; Protein; 531 AA.
AC	ID	AAW43749;
XX	DT	11-FEB-2000 (first entry)
XX	DT	26-FEB-1999 (first entry)
DE		Mouse bispecific antibody variant OKT3/anti-CD19 protein.
XX		
KW		OKT3; monoclonal antibody; MAb; point mutation; transplant rejection; organ recipient; diagnosis; tumour; therapy; diabody; anti-CD19; anti-CD3.
KW		
OS		Mus sp.
OS		Syntactic.
XX		
PN		DE19721700-C1.

19-NOV-1998.  
 23-MAY-1997; 97DE-1021700.  
 23-MAY-1997; 97DE-1021700.  
 (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 Kipriyanov S, Little M, Moldenhauer G;  
 WPI; 1998-596150/51.  
 N-PSDB; AV73337.  
 Monoclonal antibody OKT3 with point-mutation - where cysteine is  
 XX  
 FH  
 FT Peptide 1..19  
 FT /note= "signal peptide"  
 FT Peptide 28..138  
 FT /note= "VL-CD19 peptide"  
 FT Peptide 154..277  
 FT /note= "VR-CD19 peptide"  
 FT Peptide 283..401  
 FT /note= "VH-CD3 peptide"  
 FT Peptide 420..525  
 FT /note= "VL-CD3 peptide"  
 FT Peptide 525..531  
 FT /note= "His tag"

This sequence represents a protein which has anti-CD19 activity and is encoded by a monoclonal antibody (MAB) diabody derived from OKT3 with a point-mutation where Cys at position H100A is replaced with another polar amino acid, in this example Ser. The diabody encodes two OKT3 proteins, one which has anti-CD19 activity and one with anti-Cu2+ activity. The MAB is used in lowering or eliminating the transplant rejection in an organ recipient and for diagnostic methods for tumours and tumour therapy.

**Disclosure; Fig 3; 8pp; German.**

Sequence	XX	PN	W09924440-A1.	
288 AA;	XX	PD	28-OCT-1999.	
	XX	PF	99WO-EP02693.	
	XX	PR	21-APR-1998;	
	XX	PA	98EP-0107259.	
	XX	PA	(DOER/) DOERKEN B.	
	XX	PA	(RIET/) RIETHMUELLER G.	
	PI	Kufner P., Lutterbuese R,	Bargou R,	Loeffler A;
	XX			

Query Match	78.7%; Score 1208; DB 19; Length 288;	DR	N-PSDB; AAZ30332.
Best Local Similarity	78.7%; pred. No. 4; e-71;	XX	
Matches	233; Conservative 17; Mismatches 33; Indels 13; Gaps 2;	PT PT	Novel multifunctional polypeptide for treating B-cell malignancies especially non-Hodgkin lymphoma

PS Example 2; Fig 8; 91PP; English.  
 XX  
 CC The present sequence represents a bscCD19xCD3 antibody. This antibody  
 CC is a bispecific single-chain polypeptide comprising domains providing  
 CC binding-site of immunoglobulin chains and antibodies specifically  
 CC recognizing CD19 and CD3 antigen. The polypeptide destroys CD19 positive  
 CC target cells without any need of T-cell pre and/or co-stimulation, by  
 CC recruiting cytotoxic T-lymphocytes and so specific lysis by T-cells.

236 EADDAATYCCQWSSNPFTFGSGTKEINRADATPGSEQLISEEDLNSHHHHH 291  
 | |||| : ||| : ||||| ||| | ||||| ||||| |||||  
 233 e k v d a t y n c q s t e d p w t f g g t k l e i k r a d a a a g s e q k l i s e e d l n s h h h n 288

cc cc  
 cc cc  
 cc cc  
 cc cc  
 cc cc  
 inhibiting viral diseases by preventing viral infection.

Sequence 531 AA;

Best Local Similarity 80.3%; Pred. No. 8.1e-66; Mismatches 25; Indels 22; Gaps 2; Matches 217; Conservative

Query Match 65.8%; Score 1010.5; DB 20; Length 281;

Oy 82 YNOKEKDAAKLTDXSSTSAYMQLSLTSEDSAVYCARYDDHYSLDYNGQGTILTVSS 141  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 342 ynqkfkdakattdksstamqslsitsedsavycaryddhyclwyngqtltvs 401  
Oy 142 AKTPKLEEGESEARV-DIVLQTQSAAIMSPGAEVUTMCASSVSYWNYQOKSGT 200  
: ;  
Db 402 vegggsgsgsgsgsgvadllqtlqgtapaimaspgkvektmtcrassvsvnwyyqkgsts 461  
Oy 201 PKRWIYDTSKLASGVPAHFRSGSGTSYSLITISGMAEDAATYCOQWNSNPTFGSGTK 260  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Dg 462 pkrwiydtksvasgypyrfsqsgsgtsystisltisnaedadatyycqgwssnplifgakt 521

Qy 180 TCSASSSSVMWVQOKSGSPKRIVYDVKLASCQVPAHRRGSGCOTSYTIS  
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
 179 TCSASSSSVMWVQOKSGSPKRIVYDVKLASCQVPAHRRGSGCOTSYTIS  
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I

RESULT  
AAW82744 7

RESULT 8

XX  
DT  
XX  
DE  
Fusion protein pIC1266/8061scFvtaq/his.  
10-MAY-1999 (first entry)

XX  
DT  
XX  
25 - JUN - 2001 (first entry)

conjugate; cell targeting; cyclooxygenase; plasmid; fusion protein; KW prod ring-converting enzyme; cell surface antigen; treatment; cancer; inflammation; rheumatoid arthritis; antibody; prodrug therapy system. OS XX  
XX Synthetic.

KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID; KW acquired immune deficiency syndrome; severe combined immune deficiency; KW T cell lymphoma; fusion construct.

05-MAY-1998; 98WO-GB012941  
10-MAY-1997; 97GB-0009421  
(ZENE ) ZENeca LTD.  
Blakey DC, Emery SC;  
WPI; 1999-059700/05.  
N-PSDB; AAV2069.

New gene construct expressing conjugate of targeting agent and prodrug-converting enzyme - useful for, e.g. targeted production of cytotoxic drug *in vivo*, especially for treatment of cancer

CC  
CC This sequence is used in a method for obtaining a novel gene construct  
CC which expresses, in cells of a mammal, a conjugate (B) of a  
CC cell-targeting group (I) and a heterologous prodrug-converting enzyme  
CC (II), and (B) is directed to leave the cell for selective localisation  
CC at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a  
CC target site, specifically for treating cancer but also inflammation  
CC cytotoxic drug, then administration of (III) is used for targeted release of







XX DR WPI: 2000-36371/31.  
 XX DR PT N-PSDB; AAA10398.  
 XX PT Construct encoding recombinant scFv-toxin fusion protein to selectively  
 XX kill cells bearing antigens or receptors comprises DNA segment -  
 XX PS Claim 9; Columns 9-12; 14pp; English.  
 CC This sequence represents a recombinant single chain antibody  
 CC fusion protein anti-Tac(Fv)-PE40, which comprises the heavy and  
 CC light chain variable regions (VH and VL) of anti-rac antibody and  
 CC residues 253-613 of Pseudomonas exotoxin (PE). The anti-Tac single chain  
 CC antibody component of the immunotoxin binds to the p55 subunit (Tac  
 CC antigen) of the interleukin-2 (IL-2) receptor, which is present in large  
 CC amounts on helper T-lymphocytes. This enables the cytotoxic action of  
 CC PE40 to be targeted to these and other cell types which express the IL-2  
 CC receptor. The recombinant immunotoxin of the invention may be used to  
 CC treat a variety of autoimmune diseases, including graft-versus-host  
 CC disease, organ transplant rejection, type I diabetes, multiple  
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus and  
 CC myasthenia gravis. It may also be used in the treatment of leukaemia,  
 CC and may be used *in vitro* for the elimination of harmful cells from bone  
 CC marrow before transplant. Anti-Tac(Fv)-PE40 is more active on a molar  
 CC basis than anti-Tac antibody chemically conjugated to full-length PE  
 CC (anti-Tac-PE) or to PE40 (anti-Tac-PE40).  
 Sequence 599 AA;

FT PT  
 FT PT  
 FT Misc-difference 92 /note= "encoded by CGC"  
 FT PT  
 FT Misc-difference 99 /note= "encoded by TGT"  
 FT XX  
 FT Misc-difference 105 /note= "encoded by ACA"  
 FT CC  
 FT Misc-difference 118 /note= "encoded by CAC"  
 FT CC  
 FT Misc-difference 124 /note= "encoded by GCA"  
 FT CC  
 FT Misc-difference 148 /note= "encoded by GCG"  
 FT CC  
 FT Misc-difference 175 /note= "encoded by CGC"  
 FT CC  
 FT Misc-difference 177 /note= "encoded by GTC"  
 FT CC  
 FT Misc-difference 197 /note= "encoded by GCA"  
 FT XX  
 FT Misc-difference 202 /note= "encoded by TAG"  
 FT PT  
 FT Misc-difference 282 /note= "encoded by GGC"  
 FT PT  
 FT Misc-difference 298 /note= "encoded by ATG"  
 FT PT  
 FT Misc-difference 307 /note= "encoded by GGC"  
 FT PT  
 FT Misc-difference 308 /note= "encoded by AGC"  
 FT PT  
 FT Misc-difference 327 /note= "encoded by AGG"  
 FT PT  
 FT Misc-difference 348 /note= "encoded by CCG"  
 FT PT  
 FT Misc-difference 377 /note= "encoded by GAC"  
 FT PT  
 FT Misc-difference 394 /note= "encoded by ACC"  
 FT PT  
 FT Misc-difference 401 /note= "encoded by GAC"  
 FT PT  
 FT Misc-difference 436 /note= "encoded by ATG"  
 FT PT  
 FT Misc-difference 440 /note= "encoded by TAT"  
 FT PT  
 FT Misc-difference 497 /note= "encoded by TTG"  
 FT PT  
 FT Misc-difference 509 /note= "encoded by CGG"  
 FT PT  
 FT Misc-difference 545 /note= "encoded by GCG"  
 FT PT  
 FT Misc-difference 548 /note= "encoded by CAG"  
 FT PT  
 FT Misc-difference 562 /note= "encoded by GGC"  
 FT PN  
 XX US5863745-A.  
 XX  
 XX PD  
 XX 26-JAN-1999.  
 XX  
 PF 05-JUN-1995; 95US-0461825.

XX  
 PR 21-APR-1989; 89US-0341361.  
 PR 24-SEP-1986; 86US-0911227.  
 PR 08-APR-1992; 92US-0865722.  
 PR 05-JUN-1995; 95US-0461825.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Chaudhary VK, Fitzgerald DJ, Pastan IH, Queen CL;  
 PI Waldmann TA;  
 XX  
 DR WPI; 1999-131300/11.  
 DR N-PSDB; AAX00812.

XX  
 PT Killing cells with immunotoxin - comprising recombinant fusion protein of antibody Fv fragment and truncated Pseudomonas exotoxin  
 XX  
 PS Disclosure; Columns 9-12; 14pp; English.

The invention relates to recombinant antibody toxin fusion proteins which selectively kill cells bearing appropriate antigens or receptors. Killing cells with immunotoxin comprises contacting cells targeted to be killed with an antibody-PE40 recombinant fusion protein, where the antibody is a single-chain Fv fragment and the PE40 is a Pseudomonas exotoxin (PE) fragment that lacks amino acids 1-252 and which has at least the translocating and ADP-ribosylating activity of PE, where the cells targeted to be killed have receptors or antigens to which the antibody binds and the fusion protein has lower toxicity to cells that lack such receptors or antigens. The present sequence represents an anti-Tac(Fv)-PE40 fusion protein encoded by a Vn-Vl-linker-PE40 DNA segment.

XX  
 Sequence 59 9 AA:

Query	Match	Score	DB	Length
Best	Local Similarity	62.0%	20;	599;
Matches	Conservative	76.3%; Pred. No. 3.9e-54;		
	Mismatches	8; Indels	47;	
		Gaps	5;	
		2;		
OY	23 QVQLOOSGAELARPACASVVKMSCKASGYTFRYTMWIKWKRQPGGLEWGGYINPSRGTYN	82		
Db	2 qvqlqsgaelakpgpsvknscasgtyftsyrmhvwkrgpglewqyinpstgyley	61	..	
OY	83 NQFKDKAKLTIDKSSSTAYMQLSLSITSDSAVYCARYDDHVSLLDWQGQTLLVSSA	142		
Db	62 nqfkdkakltidksstaymqlslltfsavycar--gggvdwyqgqtltvssg	118	..	
OY	143 KTPPKLEEGFSEARVDIVITQSPAMSPSGEKVTMTCASSVSYMMWYQOKSGTR	202		
Db	119 gggs-gggsgggsgsqvltsqpsaimssaspgekvttassassisymhwfqkpktpk	176		
OY	203 RWIYTTSKIALSGVPFHFRSGSGHSYSLITSGMEREDAATYCCOWSSNPFTFGSGTKIE	262		
Db	177 lwyttsnlasgvparfsqsgsgsqtyslystisrmeadaatcyychqrstyptifsgtkle	236		
OY	263 INRADATAPIGSEQ	275		
Db	237 lkggslaaltahq	249		

Search completed: March 5, 2002, 17:05:34  
 Job time: 32 sec

Wed Mar 6 05:48:53 2002

us-09-424-705-2.rag

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Run on: March 5, 2002, 17:05:02 ; Search time 16.04 Seconds  
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OM protein - protein search, using sw model

Title:	US-09-424-705-2						
Sequence:	1 MKYLIFTAAGLLILRAQPA.....GSEQLKISEEDLNSHHHHH 291						
Scoring table:	BLOSUM62						
Gapext:	Gapext 0.5						
Searched:	219241 seqs, 76174552 residues						
Number of hits satisfying chosen parameters:	219241						
Minimum DB seq length:	0						
Maximum DB seq length:	200000000						
Post-processing:	Maximum Match 0% Listing first 45 summaries						
Database :	PIR_68.* 1: pir1: 2: pir2: 3: pir3: 4: pir4:  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES							
Result No.	Score	Query Match Length	DB ID	Description			
1	857.5	55.8	268	A56446	RESULT 1		
2	671	43.7	249	S41374	A56445 19 heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)		
3	612	39.8	233	JC5322	C;Species: Mus musculus (house mouse) C;Accession: A56446 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996		
4	545	35.5	144	B30502	R;Range: P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.		
5	540.5	33.2	139	2 PS0024	J. Biol. Chem. 270, 7829-7835, 1995		
6	531	34.6	235	4 PC440	A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical to the Ig heavy chain pre-protein encoded by the IgM13 gene		
7	527	34.3	287	4 PC440	A;Reference number: A56446; MUID: 95229583		
8	521.5	34.0	246	2 S38950	A;Accession: A56446		
9	521.5	34.0	446	2 S40295	A;Status: preliminary		
10	519	33.8	107	1 A30526	A;Molecule type: mRNA		
11	519	33.8	474	1 G2MS11	A;Residues: 1-208 <TAN>		
12	514	33.5	107	2 B30562	A;Cross-references: GR:U20617		
13	514	33.5	130	1 JI009	C;Keywords: heterotetramer; immunoglobulin		
14	513.5	33.4	20	541394	Query Match 55.8%; Score 857.5; DB 2; Length 268: Best Local Similarity 65.3%; Pred. No. 1.1e-51; Matches 175; Conservativeness 25; - Mismatches 61; Indels 7; gaps 3; -		
15	512.5	33.4	140	2 PH1482	Qy	21 MAQVOLQSGELARGAVSMCKASGYFTRYTHWVKORPGQDLEWICYINPRGTY 80	Db 1 MAQVQLQESGAELVKRGAVSKLSTSGENIKDTYHMKWKRPEQGLEWIGRIAPANGIT 60
16	511.5	33.3	139	1 A27609	Qy	81 NYNQKDKAALTDSSSTAYMQLSLTSEDSAVYCARYDDHSLDWGQGTILTYS 140	Db 61 KVDPKIQGKATAADPSNTAYLQLSLSLTSDTAVVYCASYLTRYE-NYNGQGTIVTS 119
17	508.5	33.1	140	1 HVMSG7	Qy	141 SAKTTKLEEGEFSEARVDIVTOSAIMSAMASPGEKVTMGSASSVSVMWYQQTSGTS 200	Db 120 SGGGG-GGGDSGGSDIELTQSPLMSASLGERVMSCRASSVSFVWQQSDAS 177
18	508	33.1	103	2 S29591	Qy	201 PKRWIDTSKIASGVVAHFRGSGSCSYSLTISGMADAATYCCQWSRSPFTEGSKT 260	Db 178 PKLWVYTSHLPPGVPRFSGSGSGNSYSLTSMGEDAATYCCQFTSSPFTEGSGTK 237
19	506.5	33.0	120	2 B22769	Qy	261 LEINRADT---APTSQKLISEEDLN 284	
20	504	32.8	104	2 B49049	Db	238 LEIKRSAAHHHHHGAEQKLISEEDLN 265	
21	503.5	32.8	122	2 S24287	RESULT 2		
22	503.5	32.8	139	2 S66537	S41374	single chain Fv antibody - mouse	
23	503.5	32.8	139	1 MHMS18	C;Species: Mus musculus (house mouse)		
24	501.5	32.6	469	2 S37483	C;Accession: S41374		
25	501	32.6	106	2 PS0001	R;Artzraenko, O.; Weiler, E. W.; Muenter, K.; Conrad, U.		
26	501	32.6	120	2 S25175	A;Submitted to the EMBL Data Library, January 1994		
27	499.5	32.5	140	2 PH1489	A;Description: Construction and functional characterization of a single chain Fv anti-		
28	497.5	32.4	108	2 G30562	Ig heavy chain V		
29	497	32.4	118	2 S38565	Ig heavy chain V r		

A; Reference number: S41374	A; Accession: 541374	RESULT 4
A; Status: preliminary	A; Status: preliminary	B30502
A; Molecule type: DNA	A; Molecule type: DNA	19 heavy chain V region (D444) - mouse
A; Residues: 1-249 <ART>	A; Residues: 1-249 <ART>	Ig heavy chain V region (D444) - mouse
A; Cross-references: EMBL:Z29480	A; Cross-references: EMBL:Z29480	Ig heavy chain V region (D444) - mouse
Query Match 43.7%; Score 671; DB 2; Length 249;	Query Match 43.7%; Score 671; DB 2; Length 249;	C; Species: Mus musculus (house mouse)
Best Local Similarity 56.0%; Pred. No. 5.3e-39; Mismatches 140; Conservative 29; MisMatches 73; Indels 8; Gaps 2;	Best Local Similarity 56.0%; Pred. No. 5.3e-39; Mismatches 140; Conservative 29; MisMatches 73; Indels 8; Gaps 2;	C; Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
Qy 23 QVOLQSGAELARPAGSVKMSCKASGYTTRTMHWKQRPGOGLEWIGYINPSRGYTN 82	Qy 23 QVOLQSGAELARPAGSVKMSCKASGYTTRTMHWKQRPGOGLEWIGYINPSRGYTN 82	C; Accession: B30502
Db 1 QVOLQSGAELARPAGSVKMSCKASGYTTRTMHWKQRPGOGLEWIGYINPSRGYTN 82	Db 1 QVOLQSGAELARPAGSVKMSCKASGYTTRTMHWKQRPGOGLEWIGYINPSRGYTN 82	R; Eliat, D.; Webster, D. M.; Rees, A. R.
Qy 83 NQKFKDQATLTDKSSSTAYMOLSLTSEDSAVYCARYYDDHYSLYWGQGTITLVSSA 142	Qy 83 NQKFKDQATLTDKSSSTAYMOLSLTSEDSAVYCARYYDDHYSLYWGQGTITLVSSA 142	J. Immunol. 141, 1745-1753, 1988
Db 179 PGQSPQQLIYRNLASCVPDRPSGSGSTSFTLRISRAEADVGVYVCMQHREYPLTEG 238	Db 179 PGQSPQQLIYRNLASCVPDRPSGSGSTSFTLRISRAEADVGVYVCMQHREYPLTEG 238	A; Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
Qy 257 SGTKLEINRA 266	Qy 257 SGTKLEINRA 266	A; Reference number: A30502; MUID:8315787
Db 239 AGTKLEIKRA 248	Db 239 AGTKLEIKRA 248	A; Accession: B30502
RESULT 3	RESULT 3	A; Status: preliminary
JC5322	JC5322	A; Molecule type: mRNA
p53 specific single-chain antibody Pab421 - human	p53 specific single-chain antibody Pab421 - human	C; Keyword: heterotetramer; immunoglobulin
C; Species: Homo sapiens (man)	C; Species: Homo sapiens (man)	C; Superfamily: immunoglobulin homology <IMM>
C; Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997	C; Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997	F; 15/98/Domain: Immunoglobulin homology
R; Jannöt, C.B.; Hynes, N.E.	R; Jannöt, C.B.; Hynes, N.E.	A; Residues: 1-144 <ETL>
Biochem Biophys Res Commun 230, 242-246, 1997	Biochem Biophys Res Commun 230, 242-246, 1997	C; Keyword: heterotetramer; immunoglobulin
A; Title: Characterization of scFv-421, a single-chain antibody targeted to p53.	A; Title: Characterization of scFv-421, a single-chain antibody targeted to p53.	C; Superfamily: immunoglobulin homology <IMM>
A; Reference number: JC5322	A; Reference number: JC5322	A; Molecule type: mRNA
A; Accession: JC5322	A; Accession: JC5322	A; Residues: 1-233 <JAN>
A; Experimental source: hydroloma cell	A; Experimental source: hydroloma cell	A; Comment: This protein specifically binds the tumor suppressor protein p53. It restores
Comment: This protein specifically binds the tumor suppressor protein p53. It restores	Comment: This protein specifically binds the tumor suppressor protein p53. It restores	A; Title: Experimental source: hydroloma cell
RESULT 5	RESULT 5	A; Accession: PS0024
PS0024	PS0024	Tg heavy chain precursor V region (6A4) - mouse
Query Match 39.8%; Score 612; DB 2; Length 233;	Query Match 39.8%; Score 612; DB 2; Length 233;	C; Species: Mus musculus (house mouse)
Best Local Similarity 53.6%; Pred. No. 5.3e-35; Mismatches 133; Conservative 26; MisMatches 63; Indels 26; Gaps 5;	Best Local Similarity 53.6%; Pred. No. 5.3e-35; Mismatches 133; Conservative 26; MisMatches 63; Indels 26; Gaps 5;	C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
Qy 27 QOSGAELARPAGSVKMSCKASGYTFRTRTMHWKQRPGOGLEWIGYINPSRGYTNQKF 86	Qy 27 QOSGAELARPAGSVKMSCKASGYTFRTRTMHWKQRPGOGLEWIGYINPSRGYTNQKF 86	C; Accession: PS0024
Db 1 QESGAELYRSGAVSKLSCTSTGFNINDYMMHWKKRPEQGLEWIGRIDPENGADMTRS 60	Db 1 QESGAELYRSGAVSKLSCTSTGFNINDYMMHWKKRPEQGLEWIGRIDPENGADMTRS 60	R; Magert, M.; Erhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Qy 87 KDKATLUTDKSSSTAYMOLSLTSEDSAVYCARYYDDHYSLYWGQGTITLVSSAKITP 146	Qy 87 KDKATLUTDKSSSTAYMOLSLTSEDSAVYCARYYDDHYSLYWGQGTITLVSSAKITP 146	A; Title: Cloning and characterization of cDNAs coding for the heavy and light chains
Db 61 GVKATWADTSNTAYQQLSSTEDAVYCC-----NAGMYWQGQTIVTWSGG-----110	Db 61 GVKATWADTSNTAYQQLSSTEDAVYCC-----NAGMYWQGQTIVTWSGG-----110	A; Reference number: PS0023; MUID:89232725
Qy 147 KLEEGEFSEARV-----DIVLQSPAIMSASPGEKYTMCSASSV----SYMWQ 195	Qy 147 KLEEGEFSEARV-----DIVLQSPAIMSASPGEKYTMCSASSV----SYMWQ 195	A; Molecule type: mRNA
Db 111 ---GGGSGGRASGGSDIELTQSPASLAVISQORATISCRASKSYSTGSYMHWNHQ 166	Db 111 ---GGGSGGRASGGSDIELTQSPASLAVISQORATISCRASKSYSTGSYMHWNHQ 166	A; Residues: 1-39 <MAR>
Qy 196 KSGTSPKRWVYPTSKLASVGPAPHRGGSGSTSVLTSIGMEARDAAATVYQDQMSNNPMP 255	Qy 196 KSGTSPKRWVYPTSKLASVGPAPHRGGSGSTSVLTSIGMEARDAAATVYQDQMSNNPMP 255	C; Experimental source: strain BALB/C
Db 167 KPGOPPRPLLIYLVNLESQGPAPRSGSGGTDETLNINHVEEADAYYCQHIRELRTSE 226	Db 167 KPGOPPRPLLIYLVNLESQGPAPRSGSGGTDETLNINHVEEADAYYCQHIRELRTSE 226	C; Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomonas aeruginosa. It is a single-chain antibody.
Qy 256 GSGTKEI 263	Qy 256 GSGTKEI 263	C; Superfamily: immunoglobulin V region; immunoglobulin homology
Db 227 G-GTKLEI 233	Db 227 G-GTKLEI 233	C; Keywords: heterotrimer; immunoglobulin; pyroglutamic acid
Query Match 35.2%; Score 540.5; DB 2; Length 139;	Query Match 35.2%; Score 540.5; DB 2; Length 139;	F; 1-19/Domain: signal sequence #status predicted <SRG>
Best Local Similarity 84.3%; Pred. No. 2.2e-30; Mismatches 102; Conservative 8; MisMatches 10; Indels 1; Gaps 1;	Best Local Similarity 84.3%; Pred. No. 2.2e-30; Mismatches 102; Conservative 8; MisMatches 10; Indels 1; Gaps 1;	F; 20/Domain: 19 heavy chain V region #status predicted <IGV>
Qy 22 AQVOLQSGAELARPAGSVKMSCKASGYTTRTMHWKQRPGOGLEWIGYINPSRGYTN 81	Qy 22 AQVOLQSGAELARPAGSVKMSCKASGYTTRTMHWKQRPGOGLEWIGYINPSRGYTN 81	F; 20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
Db 19 SQVOLQSGAELAKGAGSVKMSCKASGYTTRAYMWKQRPGOGLEWIGYINPSRGYTN 78	Db 19 SQVOLQSGAELAKGAGSVKMSCKASGYTTRAYMWKQRPGOGLEWIGYINPSRGYTN 78	F; 20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
Qy 82 YNQKFKDQATLTDKSSSTAYMOLSLTSEDSAVYCARYYDDHYSLYWGQGTITLVSS 140	Qy 82 YNQKFKDQATLTDKSSSTAYMOLSLTSEDSAVYCARYYDDHYSLYWGQGTITLVSS 140	F; 20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
Db 79 YNQKFKDQATLTDKSSSTAYMOLSLTSEDSAVYCARYYDDHYSLYWGQGTITLVSS 138	Db 79 YNQKFKDQATLTDKSSSTAYMOLSLTSEDSAVYCARYYDDHYSLYWGQGTITLVSS 138	F; 20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

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### OM protein - protein search, using sw model

Run on:

March 5, 2002, 17:05:57 ; Search time 12.93 Seconds

(without alignments)

825.171 Million cell updates/sec

Title: US-09-424-705-2

Perfect score: 1536

Sequence: 1 MYLLPPTAAGLILLAAQPA. .... GSEQKLISEEDLNHHHHH 291

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

To number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

**pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	RESULT ID	RT	RL	CC
1	508.5	33.1	140	1 HV02_MOUSE	P01746 mus musculu	HV02_MOUSE	STANDARD;	PRT;	PRR; 140 AA.
2	508	33.1	120	1 HVV3_MOUSE	P01747 mus musculu	P01746;			
3	503.5	32.8	139	1 HV02_MOUSE	P01751 mus musculu	21-JUL-1986 (Rel. 01, Created)			
4	500	32.6	107	1 KV5F_MOUSE	P04940 mu musculu	21-JUL-1986 (Rel. 01, Last sequence update)			
5	497	32.4	107	1 KV5J_MOUSE	P04944 mu musculu	15-JUL-1999 (Rel. 38, Last annotation update)			
6	495	32.2	107	1 KV5I_MOUSE	P04943 mu musculu	IG HEAVY CHAIN V REGION 93G7 PRECURSOR.			
7	494	32.2	107	1 KV5H_MOUSE	P04942 mu musculu	MUS musculus (Mouse).			
8	491	32.0	107	1 KV5G_MOUSE	P04941 mu musculu	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID=10090; [1]			
9	482.5	31.4	137	1 HV11_MOUSE	P01755 mus musculu	RN	SEQUENCE FROM N.A.		
10	463	30.1	138	1 HV08_MOUSE	P03980 mus musculu	RP	STRAIN=F/J;		
11	462.5	30.1	120	1 HV50_MOUSE	P06329 mus musculu	RX	MEDLINE=82152818; PubMed=6801765;		
12	462	30.1	117	1 HV12_MOUSE	P01756 mus musculu	RA	Sims J.; Rabbits T.H., Estess P., Slaughter C., Tucker P.W., Capra J.D.;		
13	457	29.8	117	1 HV13_MOUSE	P01757 mus musculu	RA	"Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";		
14	446	29.0	107	1 KV5B_MOUSE	P04941 mu musculu	RT	Science 216:309-311(1982).		
15	446	29.0	121	1 HV01_MOUSE	P01755 mus musculu	CC			
16	443	28.8	117	1 KV08_MOUSE	P01675 mu musculu	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).		
17	443	28.8	117	1 HV04_MOUSE	P01678 mu musculu	CC			
18	442	28.8	107	1 KVGD_MOUSE	P01677 mu musculu	DR	EMBL; J00493; AAA38128; 1; PIR; A0228; HVM6G7.		
19	441	28.7	107	1 KVCG_MOUSE	P01745 mu musculu	DR	InterPro; IPR003006; Ig_MHC.		
20	440	28.6	136	1 HV15_MOUSE	P01676 mu musculu	DR	InterPro; IPR003396; Ig_V.		
21	436.5	28.4	117	1 HV01_MOUSE	P01749 mu musculu	DR	SMART; SF00046; Ig_V.		
22	436	28.4	117	1 HV05_MOUSE	P01750 mu musculu	DR	SMART; SF00047; Ig_V.		
23	434	28.3	117	1 HV06_MOUSE	P01750 mu musculu	DR	PFam; SF00047; Ig_V.		
24	427	27.8	108	1 KV0K_MOUSE	P04945 mu musculu	DR	SMART; SF00046; Ig_V.		
25	426	27.7	117	1 HV09_MOUSE	P01753 mu musculu	DR	SEQUENCE FROM N.A.		
26	424	27.6	107	1 KV6E_MOUSE	P01679 mu musculu	FT	FT SIGNAL 1 19 IG HEAVY CHAIN V REGION 93G7.		
27	422	27.5	117	1 HV09_MOUSE	P01754 mu musculu	FT	FT NON_TER 140 140 140 MW: 25A4CBBE31DA5CE8 CRC64;		
28	420	27.3	117	1 HVIC_HUMAN	P01750 mu musculu	SEQUENCE	140 AA; 15514 MW;		
29	412.5	26.9	147	1 HVIC_HUMAN	P01744 homo sapien	QY	Query Match 33.1%; Score 508.5; DB 1; Length 140; Best Local Similarity 74.4%; Pred. No. 2e-33; Matches 99; Conservative 9; Mismatches 22; Indels 3; Gaps 2;		
30	411	26.8	117	1 HV72_MOUSE	P06327 mu musculu	QY	12 LFLILAAQPAM-AQVOLQOSGAELARPAGSKMSKASGYTFRTYRMWYKQPGGLEWI 70		
31	410.5	26.7	117	1 HV14_MOUSE	P01758 mu musculu	Db	8 LFLISVTPVGHSEVOLQOSGAELVRAGSVSKMSKASGYTFRTYRMWYKQPGGLEWI 67		
32	407	26.5	129	1 KVKA_MOUSE	P01680 mu musculu	Db	71 GYINPSRGTYNTNQKFQDKATUTDKSSSTAYMQLSSTESDAYSVCAR--YDDHSL 128		
33	399	25.3	117	1 HVIB_HUMAN	P01743 homo sapien	QY	68 GYINPQNGYVNTNEKEFKTTLTVDKSSTAVMQLSLSDESAVECARHYGGSYDF 127		

MAKING ANTIBODIES TO THE HAPten (4-HYDROXY-3-NITROPHENYL)ACETYL (NpB ANToBODIES)	
RV03_MOUSE	RESULT 2
ID RV03_MOUSE	hv03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;	PO1747; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)	DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.	DE
OS Mus musculus (Mouse); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OS
OC NCBI_TaxID=10090;	OC
OX OX [1]	OX
RN RP SEQUENCE FROM N_A.	RN
PB MEDLINE=83131846; PubMed=6186498; Siekavitz, M.; Geitler, M.L.; Brodeur, P.; Riblet, R.; Marshak-Rothstein, A.; "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse."; Eur. J. Immunol. 12:1023-1032(1982).	PB
RL -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J GENE. SEGMENT, JH2.	RL
DR PIR; A02028; HVMSGT; InterPro; IPR000066; Ig_MHC.	DR
DR InterPro; IPR003596; Ig_V.	DR
DR InterPro; IPR003596; Ig_V.	DR
DR Pram; PF00047; Ig_V.	DR
DR SMART; SM00406; Ig_V.	DR
DR Immunoglobulin_V_region; Antiarsonate antibody; Hybridoma.	DR
KW Immunoglobulin V region; Ig_V.	KW
FT Immunoglobulin_V_region; signal.	FT
FT SIGNAL 1 19	FT
FT CHAIN 20 139	FT
FT DOMAIN 20 49	FT
FT DOMAIN 50 54	FT
FT DOMAIN 55 68	FT
FT DOMAIN 69 85	FT
FT DOMAIN 86 117	FT
FT DOMAIN 118 124	FT
FT DOMAIN 125 139	FT
FT DISULFID 41 115	FT
FT NON_TER 139 139	FT
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;	SQ
Query Match 33.1%; Score 508; DB 1; Length 120; Best Local Similarity 80.8%; Pred. No. 1.8e-33; Matches 97; Conservative 5; Mismatches 16; Indels 2; Gaps 1;	Query Match 32.8%; Score 503.5; DB 1; Length 139; Best Local Similarity 74.8%; Pred. No. 4.8e-33; Matches 101; Conservative 9; Mismatches 18; Indels 7; Gaps 3;
QY 24 VOLQQSAGELARPGASVYKMSCKASGVTFRTRYTMHWKQQRPGGLEWGYINPSRGVINYNN 83	QY 12 LLLIAAQP-AMAOVQLOQSAGELARPGASVYKMSCKASGVTFRTRYTMHWKQQRPGGLEWGYINPSRGVINYNN 83
Db 1 QVKFDKATLTDKSSTAYMQQLSLSITSEDAVYCCAR--YYDHYSLDYWGMGGTTLVSS 141	Db 7 MFLATATGVSQVHQVSLQDQGAELVKPGASVYKMSCKASGVTFRTRYTMHWKQQRPGGLEWGYINPSRGVINYNN 66
QY 84 VOLQQSAGELVRAGSSVYKMSCKASGVTFRTRYTMHWKQQRPGGLEWGYINPSRGVINYNN 60	QY 67 IGRIDPNSSGTKEKFKSATLTVDKSSTAYMQQLSLSITSEDAVYCCAR--YYDHYSLDYWGMGGTTLVSS 124
Db 121 EFKFGKTTITDQSSTAYMQQLSLSITSEDAVYCCAR--YYDHYSLDYWGMGGTTLVSS 120	Db 128 -LDYWGMGGTTLVSS 141
RESULT 3	RESULT 4
HV07_MOUSE	KV6F_MOUSE
ID HV07_MOUSE	STANDARD; PRT; 139 AA.
AC P01751; P01752;	AC P017540;
DT 21-JUL-1986 (Rel. 01, Created)	DT 13-AUG-1987 (Rel. 05, created)
DT 21-JUL-1986 (Rel. 01, last sequence update)	DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)	DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.	DE IG KAPPA CHAIN V-VI REGION NQ2-17.4.1.
OS Mus musculus (Mouse); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OS Mus musculus (Mouse); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;	OC NCBI_TaxID=10090;
OX OX [1]	OX
RN RP SEQUENCE FROM N_A.	RN
PB MEDLINE=81234548; PubMed=6788376; STRAIN=C57BL/6; RT	PB MEDLINE=83271467; PubMed=6877353; RT
RC Baltimore D.; Paskind M., Imanishi-Kari T., Rajewsky K., RT	RC Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.; RT
RA Bothwell A.L.M., Paskind M., Imanishi-Kari T., Rajewsky K., RT	RA "mRNA sequences define an unusually restricted IgG response to 2-phenoxyloazolone and its early diversification.";
RA Baltimore D.; Paskind M., Imanishi-Kari T., Rajewsky K., RT	RA Nature 304:320-324 (1983).
RT Heavy chain variable region contribution to the NpB family of antibodies: somatic mutation evident in a gamma 2a variable region.";	RT !- FUNCTION: ANTI-2-PHENYL OXAZOLE (PHOX) ANTIBODY.
RL Cell, 24:625-637(1981).	RL
CC !- MISCELLANEOUS: THE B1-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA	CC This SWISS-Prote entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

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## OM protein - protein search, using sw model

Run on:

March 5, 2002, 17:05:37 ; Search time 24.4 Seconds

(without alignments)  
1744.477 Million cell updates/sec

Title: US-09-424-705-2  
Perfect score: 1536  
Sequence: 1 MKYUJPTAAAGLLLAAQPA.....GSEOKLISEBDLNSHHHHH 291

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

T number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL17;\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rabbit:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT	1
0QYF0	PRELIMINARY;
0QYF0	PRT;
AC 0QYF0;	298 AA.
DT 01-MAY-2000 ( TREMBrel. 13, Created)	--
DT 01-MAY-2000 ( TREMBrel. 13, Last sequence update)	--
DT 01-JUN-2001 ( TREMBrel. 17, Last annotation update)	--
DE CN 8 SCFV.	--
GN OS	--
OC MUS musculus (Mouse).	--
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	--
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus;	--
RN NCBI_TAXID=10090;	[1]
RP SEQUENCE FROM N.A.	
RC STRAIN=BALB/C; TISSUE=SPLEEN;	
RA Shinohara N., Demura T., Fukuda H.;	
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.	

[2]

SEQUENCE FROM N.A.
RA Shinohara N., Demura T., Fukuda H.;
RT "ISOLATION OF A NOVEL TYPE OF VASCULAR CELL WALL-SPECIFIC MONOCLONAL ANTIBODY RECOGNIZING A CELL POLARITY USING A PHAGE DISPLAY SUBTRACTION METHOD";
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN
DR EMBL; AB036341; BA88633; 1; -.
DR HSSP; P01607; IRET;
DR InterPro; IPR03005; Ig_MHC.
DR InterPro; IPR03596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0T96B0A17004317 CRC64;

Query Match 44.9%; Score 690; DB 11; Length 298;  
Best Local Similarity 54.7%; Pred. No. 4.9e-50;  
Matches 139; Conservative 35; Mismatches 72; Indels 8; Gaps 5;

Searched: 473505 seqs, 146272329 residues

T number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Query Match 44.9%; Score 690; DB 11; Length 298;  
Best Local Similarity 54.7%; Pred. No. 4.9e-50;  
Matches 139; Conservative 35; Mismatches 72; Indels 8; Gaps 5;

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Post-processing:

Db	33	AAGPAMADQVKLQDGGGLVKGPGSSKLKCAASGSDFSRWMWSWROAPGKGLWEIGEINP	92	AC	Q99L25;	
Db	76	SRGYTNWQKKOKATLTDKSSSTAYMOLSSLTSEDAVYCAR--VYDDHVSLSYMQ	133	DT	01-JUN-2001 (TREMBlrel. 17, last sequence update)	
Db	93	DSSTINYTPSLKBFILSRDNKNTLYLOMSKVRSEDALIYCARASY--GHSAA--YNGQ	149	DT	01-JUN-2001 (TREMBlrel. 17, last annotation update)	
Db	134	GTRLVVSAKTPKLEGEFSEARVDIVLTOAPSIAIMSASPGEKVTMCASSSV-SYNN	192	DE	SIMILAR TO RIKEN CDNA 1810060009 GENE.	
Db	150	GTRVTVSSGGGS--GGCGGGSDIELTOSPLASAVGETVITCRASNINHLY	207	OS	Mus musculus (Mouse).	
Qy	193	YQQSGTSKPRWYDTSKLASGVPAHFQSGSGTSYSLTISGMEDAATYYCQWSSNP	252	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Db	208	YQQSGTSKPOLLYNAKTLADGVSPRSFSGSGSQYQSKINSLOPEDRGSYYCQHEWTIP	267	OC	EMBL; BC003888; AAH03888.1; -. BE5889B7986DA155 CRC64;	
Qy	253	FTFGGGTKEINRA	266	DR	SEQUENCE FROM N.A.	
Db	268	YTFGGGTKEINRA	281	DR	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	
Qy	2			RL	EMBL; BC003888; AAH03888.1; -. BE5889B7986DA155 CRC64;	
Qy	9QGYZ2	PRELIMINARY;	PRT;	119 AA.	SQ	SEQUENCE FROM N.A.
Qy	9QYZ2				Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
Db	01-MAR-2001	(TREMBlrel. 16, Created)	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;			
DT	01-MAR-2001	(TREMBlrel. 16, Last sequence update)	Matches 121; Conservative 29; Mismatches 64; Indels 50; Gaps 8;			
DT	01-JUN-2001	(TREMBlrel. 17, Last annotation update)	Matches 121; Conservative 29; Mismatches 64; Indels 50; Gaps 8;			
Db	MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION (FRAGMENT).	82 YNOKIKDKATLTTRKSSSTAYMOLSSLTSEDAVYCAR--VYD-DHYSLDWQGQT	136	Qy	Query Match 33.2%; Score 510; DB 11; Length 473;	
DE	Schistosoma japonicum (Blood fluke); Trematoda; Digenea; Rhabdophora; Neodermata; Schistosomatidae; Schistosoma; Schistosomatidae; Schistosoma japonicum.; {1}	79 YNEKFGRKATLTDKSSSTAYMOLNLSTSBDASVCCSRSQGSIVYGYLYFDWQGTT	138	Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;	
RP	SEQUENCE FROM N.A.	Qy 137 LTVSAAKTPKLEGEFSEARVDIVLTOAPSIAIMSASP---GEKVTMCASSSVSM	190	Qy	Query Match 33.2%; Score 510; DB 11; Length 473;	
RA	Song X.T., Feng Z.Q., Guan X.H.; variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum.; Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.	Db 139 ITVSAKTT-----APSVYPLAPVGDTGQSSTVLGCLVK--GYF	176	Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;	
RT		Qy 191 NWYQOKSGTSKPRWYDTSKLASGV--PAHFQSGSGTSYSLTISGMEDAATYYCQ	247	Qy	Query Match 33.2%; Score 510; DB 11; Length 473;	
RT		Db 177 -----PDPVLTWNSSGLSSGVHTFPAVLQLSDLTSSVWTT-----SSTWPQS	222	Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;	
CC	- - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	Qy 248 WSSNPFTEGSGTKIEINRADAPT	271	Qy	Query Match 33.2%; Score 510; DB 11; Length 473;	
CC	EMBL; AP282622; AAG0152.1; -.	Db 223 ITCNVAHPASSTKVDKKIEPRGPT	246	Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;	
DR	InterPro; IPR003599; Ig_1-like.	RESULT 4		Qy	Query Match 33.2%; Score 510; DB 11; Length 473;	
DR	InterPro; IPR003606; Ig_MHC.	Q9DBL4		Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;	
DR	InterPro; IPR003596; Ig_V.	ID Q9DBL4	PRELIMINARY;	Qy	Query Match 33.2%; Score 510; DB 11; Length 473;	
PFam	PF00047; Ig_1.	ID Q9DBL4	PRT;	473 AA.	DR	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
DR	SMART; SM00409; Ig_1.	AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
DR	SMART; SM00406; Ig_V_1.	AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
DR	SMART; SM00410; Ig_Like_1.	AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
FT	NON_TER 1	AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
FT	NON_TER 119	AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
SEQUENCE	119 AA;	AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
SO	13567 MW;	AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
Query Match 34.6%; Score 531; DB 5; Length 119;		Q9DBL4			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
Best Local Similarity 80.7%; Pred. No. 3.2e-37; Matches 96; Conservative 10; Mismatches 13; Indels 0; Gaps 0;		ID Q9DBL4	PRELIMINARY;		Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		ID Q9DBL4	PRT;	473 AA.	DR	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
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AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
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AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
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AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
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AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
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AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match 33.2%; Score 510; DB 11; Length 473;
AC		AC			Db	Best Local Similarity 45.8%; Pred. No. 1e-34; Mismatches 64; Indels 50; Gaps 8;
AC		AC			Qy	Query Match

ALIGNMENTS	
RESULT 1	S-08-469-486-57
Sequence 57, Application US/08469486	Patent No. 573981
GENERAL INFORMATION:	
APPLICANT: Thoegersen, Hans Christian	APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael	APPLICANT:
TITLE OF INVENTION: Improved method for the r	TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58	CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson	STREET: 225 Franklin Street
CITY: Boston	CITY:
STATE: Massachusetts	STATE:
COUNTRY: USA	COUNTRY:
ZIP: 02110-2804	ZIP:
COMPUTER READABLE FORM:	
MEDIUM TYPE: FLOPPY disk	COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS	SOFTWARE: Patientin Release #1.0, Version
SOFTWARE: #1.25	CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469, 486	
FILING DATE:	
CLASSIFICATION: 530	PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060	FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark	NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162	REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00363/002001	REFERENCE/DOCKET NUMBER: 00363/002001
TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070	TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906	TELEFAX: 617 542 8906
TELEX: 200154	TELEX: 200154
INFORMATION FOR SEQ ID NO: 57:	INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids	LENGTH: 246 amino acids
TYPE: amino acid	TYPE: amino acid
STRANDEDNESS:	STRANDEDNESS:
TOPOLOGY: linear	TOPOLOGY: linear
MOLECULE TYPE: protein	MOLECULE TYPE: protein
S-08-469-486-57	S-08-469-486-57

Best Local Similarity	74.5%	Pred.	No.	1e-67;	Mismatches	17;	Indels	18;	Gaps
Matches	196;	Conservative							
23	OQVLOOGSAELRPGAVSKMSCKASGYTFTRYTMHVKQRPQGLEWIGYINPSRGTYN	8	2						
1	QVKLQOOGAELRPGAVSKMSCKASGYTFTRYTMHVKQRPQGLEWIGYINPSRGTYN	60	1						
83	NQKFKDKATLTDKSSSTAYMQLSSLTSEDASAVYCAR-YVDHDYSLDYNGQGTLLVSS	141	8						
61	NEBKFSKATLTDLTDSSTASYMQLSSLTSEDASAVYCCSRGDGSDYYAMDYWGQGTIVSS	120	6						
142	AKTTPKLEEGEESEARVDIVITQSPAIMSASGEKEVITMCSCASSSYIMWVYQQSGTSP	201	1						
121	G-----GGGS---DIETLQSPAILSASPQGKVMTCGASSSYWMMWYQKPGSSP	168	1						
202	KRWIYDTSKLAAGSVPAHFRRGSGSGTSYSLTISGMEDAATYCYCOOWSSNFTFGSGTKL	261	7						
169	KFWIYATSNLASGVPRFSGSGTSYSLTISRVEEDAATYCYCOOWSRNFITFGSGTKL	228	7						
262	EINRADTAPTGSEQKLISEEDLN	284	1						
229	EIKRA----AAEQKLISEEDLN	246	1						

Query	Match	Score	DB	Length
QY	3 QVOLQSGELARPAGASWKMSCIASGYFTTRYMHWKORPGGLEWIGYINPSRGYTNW	63.4%	2;	246;
	:     :     :     :     :     :     :     :     :     :     :     :	Best Local Similarity	74.5%	Pred. No. 1.2e-67;
	1 QVKLQQSGAELVRPGASTKMSCKASGYTFASYWNWVKRPGQLEWIGYHIVPYSRITY	74.5%	32;	Mismatches
Db	83 NQFKDKATLTQKSSSTAYMQLSLSLTSDSAVIDCARYYYDHSYSLDWGQGTTLTVSS	60	17;	Conservative
QY	61 NEFKSKATLTDTSSSTAYMQLSLSLTSDSAVIDCYSRDGSDFYAMDWGOQTIVTVSS	141	17;	Mismatches
Qy	142 AKTTPKLEEGESEARVDIWLTOSPATMSASPGEKVTMCSASSSVSYNWYQQSGTSP	201	17;	196;
Db	121 G-----GGGS----DELTQSPAILASPGKRVTMCRASSSVSYHWYQQKGSSP	168	17;	196;
QY	202 KRWYDMSKCLASSVPAHHFGSGSTSYSITISGMAEDATYCQOWSSNPFFGSGTKL	261	17;	196;
Db	169 KPWYIAISNLASVPTRGSGGSTSYTISRVEADATYCQOWSNPFFGSGTKL	261	17;	196;
QY	262 EIRNADTAFTGSGBQKLSBEDLN 284	228	17;	196;
Db	229 ELKRA----AAQKLISEEDLN 246	228	17;	196;

Query	Match	Score	DB	Length
Best Local Similarity	63.4%	974	2	246
Matches	74.5%	Pred. No.	1.2e-67	
Matches 196; Conservative	17	Mismatches	32	Indels
QY	23	QVOLQSGAELARPGASVVKMSKASGVTTRTMHAWKQRPGQGLEWIGVINPSRGYTN	18	Gaps
	:     :     :     :     :     :     :     :     :     :			4;
Db	1	QVQLQQSGAELVKGPGASVVKMSKASGVTTRTMHAWKQRPGQGLEWIGVINPSRGYTN	62	
	:     :     :     :     :     :     :     :     :     :			
QY	83	NQKFKDATTIDKSSTAYMOLLSSTEDSAAVYCAR-YDDHYSLDYNGQTIVTSS	141	
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :			
Db	61	NEFKFSKATLTDTSSTAYMOLLSSTEDSAAVYCAR-YDDHYSLDYNGQTIVTSS	120	
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :			
QY	142	AKTTPKLEEGEEFSEARVDIVLITQSPAMMSASPGEKVMTCSASSSVSYMMWYQOKSGTSP	201	
	- :   :   :   :   :   :   :   :   :   :   :   :   :   :			
Db	121	G-----GGGS---DIELTQSPATLSASPGBKVTMTCRASSSYVMHWYQOKPGSSP	168	
	-----:   :   :   :   :   :   :   :   :   :   :   :   :   :			
QY	202	KRWIYDTSKLASGVPAHFRRGSGSGSYSLITSGMEREADATYCQOWSSAPFTFGSGTK	261	
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :			
Db	169	KWIYDTSKLASGVPAHFRRGSGSGSYSLITSGMEREADATYCQOWSSAPFTFGSGTK	228	
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :			
QY	262	EINRADTAPGTSEQKLISEDIN	284	
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :			
Db	229	EIKRA---AEEQKLISEDIN	246	

					GenCore version 4.5
Copyright (c) 1993 - 2000					Compugen ltd.
Run on:	March 5, 2002, 18:23:18 ;	Search time	168.12 Seconds		(without alignments)
			122.388 Million cell updates/sec		
Title:	US-09-424-705-7				
Perfect score:	24				
Sequence:	1 gtatgtcaaggctgtatgtatcatc		24		
Scoring table:	IDENTITY_NUC				
Gapov:	10.0 , Gapext 1.0				
Searched:	930621 seqs, 428662619 residues				
Number of hits satisfying chosen parameters:	1861242				
Minimum DB seq length:	0				
Maximum DB seq length:	200000000				
Post-processing:	Minimum Match 0%				
	Maximum Match 100%				
	Listing first 45 summaries				
Database :	N_Geneseq_1101:*				
1:	/SIDS1/gcadata/geneseq/geneseq/NA1980.DAT:*				
2:	/SIDS1/gcodata/geneseq/geneseq/NA1981.DAT:*				
3:	/SIDS1/gcodata/geneseq/geneseq/NA1982.DAT:*				
4:	/SIDS1/gcodata/geneseq/geneseq/NA1983.DAT:*				
5:	/SIDS1/gcodata/geneseq/geneseq/NA1984.DAT:*				
6:	/SIDS1/gcodata/geneseq/geneseq/NA1985.DAT:*				
7:	/SIDS1/gcodata/geneseq/geneseq/NA1986.DAT:*				
8:	/SIDS1/gcodata/geneseq/geneseq/NA1987.DAT:*				
9:	/SIDS1/gcodata/geneseq/geneseq/NA1988.DAT:*				
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17:	/SIDS1/gcodata/geneseq/geneseq/NA1996.DAT:*				
18:	/SIDS1/gcodata/geneseq/geneseq/NA1997.DAT:*				
19:	/SIDS1/gcodata/geneseq/geneseq/NA1998.DAT:*				
20:	/SIDS1/gcodata/geneseq/geneseq/NA1999.DAT:*				
21:	/SIDS1/gcodata/geneseq/geneseq/NA2000.DAT:*				
22:	/SIDS1/gcodata/geneseq/geneseq/NA2001.DAT:*				
					ALIGNMENTS
RESULT	1				
ID	AAV73336	standard;	DNA; 24 BP.		
XX	AAV73336;				
AC					
XX					
DT	26-FEB-1999	(first entry)			
XX					
DE	Mouse OKT3 variant antibody primer SK1 DNA.				
XX					
KW	OKT3; monoclonal antibody; Mab; point mutation; transplant rejection; organ recipient; diagnosis; tumour; therapy; primer; ss;				
XX					
OS	Synthetic.				
OS	Mus spp.				
PN					
XX	DB19721700-C1.				
XX					
PD	19-NOV-1998.				
XX					
PF	23-MAY-1997;	97DE-1021700.			
PR	23-MAY-1997;	97DE-1021700.			
XX					
PA	(DEKR-)	DEUT KREBSFORSCHUNGSZENTRUM.			
XX					
PI	Kipriyanov S, Little M, Moldenhauer G;				
XX					
DR	WPI; 1998-596150/51.				
XX					
PT	Monoclonal antibody OKT3 with point-mutation - where cysteine is replaced by another polar amino acid, useful for controlling transplant rejection, and in tumour diagnostics and therapy				
XX					
Probe #11098 for g					
Probe #15118 used					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Query	Match Length	DB ID	Description
	1	24	100.0	24	19 AAV73336
	2	24	100.0	898	19 AAV73335
	3	24	100.0	1653	21 AMZ43432
	4	24	100.0	1698	21 AMZ43431
	5	24	100.0	1794	19 AAV73337
	6	22.4	93.3	1570	12 AMQ12637
	7	22.4	93.3	1611	21 AMZ30332
	8	17.6	73.3	47	21 AMZ66503
	9	17.6	73.3	587	21 AMF08479
	10	17.4	72.5	249	22 AM121165
	11	17.4	72.5	249	22 AM146432





XX New humanised antibodies comprising CDR grafted antibody - with  
PT heavy and light chains, for use in in vivo therapy and diagnosis  
XX  
PS Disclosure; Fig 2a; 91PP; English.

CC The OK3T heavy chain sequence was isolated from a cDNA library prepared from OK3T producing cells. The library was screened with a probe complementary to a sequence in the mouse IgG2a constant CH1 domain region. The OK3T sequence was used in CDR-grafting experiments CC to prepare humanised antibodies.

XX Sequence 1570 BP; 447 A; 443 C; 356 G; 324 T; 0 other;

SQ

	Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Matches	23;	22.4;	12;	1570;	93.3%;	0;	0.23;	0;	0;	0;
1	gtagtcaaggctgtaatgatcatc	24								
Db	421	GTAGTCAGGCAGTAATGATCATC	398							

RESULT 7

ID AAZ3032/C

ID AAZ3032 standard; cDNA; 1611 BP.

XX AAZ3032;

AC AC

XX DT 11-FEB-2000 (first entry)

XX DE Nucleotide sequence of the bscCD19xCD3 antibody.

XX

KW bscCD19xCD3 antibody; bispecific single-chain fragment; CD19 antigen; CD3 antigen; CD19-positive target cell; T-cell stimulation; cytotoxic T-lymphocyte; B-cell malignancy; myasthenia gravis; cytotoxic T-lymphocyte; B-cell malignancy; myasthenia gravis; KW cytotoxic T-lymphocyte; B-cell malignancy; myasthenia gravis; KW Hashimoto thyroiditis; Goodpasture syndrome; B-cell depletion; non-Hodgkin lymphoma; gene therapy; cancer; viral disease; ds.

XX OS Synthetic.

XX

KEY Location/qualifiers

FT 11..1606

FT /\*tag= a

FT /Product= "bscCD19xCD3 antibody"

FT 11..67

FT misc\_peptide

FT /\*tag= b

FT 92..424

FT /\*tag= c

FT /note= "encode VL-CD19"

FT 470..841

FT /\*tag= d

FT /note= "encode VH-CD19"

FT 857..1213

FT /\*tag= e

FT /note= "encodes VH-CD3"

FT 1268..1585

FT /\*tag= f

FT /note= "encodes VL-CD3"

FT 1586..1603

FT /\*tag= g

FT /note= "encodes a His tag"

PN W0954440-A1.

PD 28-OCT-1999.

XX XX

PF 21-APR-1999; 99WO-EP02693.

XX S 21-APR-1998; 98EP-0107269.

PR XX

PA (DOER/ DOEREN B.

PA (RIET/ RIETHUELLER G.

PT XX

PI Kufner P., Lutterbuese R., Bargou R., Loeffler A;

XX DR WPI; 2000-013241/01.

DR P\_PSDB; RAY43749.

XX Novel multifunctional polypeptide for treating B-cell malignancies

PT especially non-Hodgkin lymphoma -

XX PS Example 2; F9 8; 91PP; English.

XX

The present sequence encodes a bscCD19xCD3 antibody. This antibody CC is a bispecific single-chain polypeptide comprising domains providing CC binding-site of immunoglobulin chains or antibodies specifically CC recognizing CD19 and CD3 antigen. The polypeptide destroys CD19-positive CC target cells without any need of T-cell pre and/or co-stimulation, by recruiting cytotoxic T-lymphocytes and so specific lysis by T-cells CC rather than a direct effect by an antibody is achieved. The bispecific CC single-chain polypeptides, or nucleotides encoding them, are used for CC the treatment of B-cell malignancies, B-cell mediated autoimmune CC diseases like myasthenia gravis, Morbus Basedow, Hashimoto thyroiditis CC or Goodpasture syndrome or for the depletion of B-cells and more CC particularly non-Hodgkin lymphoma in mammals preferably human. They can also delay the pathobiological conditions caused by these diseases, and CC can be used for detecting these diseases. The polynucleotide is used CC for gene therapy. The polypeptides are also used for identifying CC compounds modulating B-cell/T-cell mediated immune response which can in CC turn be used for treating cancer, its related diseases and also for CC inhibiting viral diseases by preventing viral infection.

XX

SQ Sequence 1611 BP; 402 A; 396 C; 440 G; 373 T; 0 other;

Query Match

	Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Matches	23;	22.4;	21;	1611;	93.3%;	0;	0.23;	0;	0;	0;
1	gtagtcaaggctgtaatgatcatc	24								
Db	1180	GTAGTCAGGCAGTAATGATCATC	1157							

RESULT 8

ID AAZ66503/c

ID AAZ66503 standard; DNA; 47 BP.

XX AAZ66503;

AC AC

XX DT 10-SEP-2001 (first entry)

XX DE Human map-related biallelic marker SEQ ID NO:850.

XX KW Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.

XX OS Homo sapiens.

XX

KEY Location/Qualifiers

FT variation

FT replace(24,c)

FT /\*tag= a

FT /standard\_name= "single nucleotide polymorphism"

XX PN W0954500-A2.

XX

PD 28-OCT-1999.

XX XX

PF 21-APR-1999; 99WO-IB00822.

XX PR 21-APR-1998; 98US-0082614.

PR 23-NOV-1998; 98US-0109732.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PT cohen D, Blumenfeld M, Chumakov I;  
 PT  
 XX DR WPI; 2000-013267/01.  
 XX  
 PT Novel biallelic markers used to construct a high density disequilibrium map of the human genome -  
 XX  
 PS Claim 1; Page 412; 2745pp; English.  
 XX  
 AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention.

SQ Sequence 47 BP; 15 A; 11 C; 5 G; 16 T; 0 other;

Query Match 73.3%; Score 17.6; DB 21; Length 47;  
 Best Local Similarity 83.3%; Pred. No. 24; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 gtatgtcaaggctgtatgtatcatc 24  
 ||||| | ||||||| ||||| ||||| 14

Db 37 GTAGTAACTGCTGTATGATGATC 14

RESULT 9  
 AAF08479  
 ID AAF08479 standard; cDNA; 587 BP.  
 AC  
 XX  
 AC AAF08479;  
 XX  
 DT 13-MAR-2001 (first entry)  
 DE Fusarium venenatum EST SEQ ID NO:1002.  
 XX  
 KW Multiple gene expression; filamentous fungal cell; EST;  
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
 KW culture condition; environmental stress; spore morphogenesis;  
 KW metabolic pathway engineering; catabolic pathway engineering; ss.  
 OS Fusarium venenatum.  
 XX  
 PN WO200056762-A2.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 22-MAR-2000; 2000WO-US07781.  
 XX  
 PR 22-MAR-1999; 99US-0273623.  
 XX  
 PA (NOVO ) NOVO NORDISK BIOTECH INC.  
 PA (NOVO ) NOVO NORDISK AS.  
 XX  
 PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
 XX

Query Match 73.3%; Score 17.6; DB 21; Length 587;  
 Best Local Similarity 83.3%; Pred. No. 38; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 gtatgtcaaggctgtatgtatcatc 24  
 ||||| | ||||||| ||||| ||||| 466

Db 443 gttgttgcgtgtatgtatcatc 466

RESULT 10  
 AAI21165  
 ID AAI21165 standard; DNA; 249 BP.  
 AC  
 XX  
 AAI21165;  
 XX  
 DT 12-OCT-2001 (first entry)  
 XX  
 DE Probe #11098 for gene expression analysis in human cervical cell sample.  
 XX  
 KW probe; human; microarray; gene expression; cervical epithelial cell;  
 KW cervical cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157278-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00670.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632466.  
 PR 21-SEPT-2000; 2000US-0234887.  
 PR 27-SEPT-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.

DR WPI; 2000-594572/56.  
 XX  
 PT Monitoring differential expression of genes in filamentous fungal cells  
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -  
 XX  
 PS Claim 86; Page 764-765; 3161pp; English.  
 XX  
 CC The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF11879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.

SQ Sequence 587 BP; 146 A; 133 C; 131 G; 172 T; 5 other;

Query Match 73.3%; Score 17.6; DB 21; Length 587;  
 Best Local Similarity 83.3%; Pred. No. 38; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 gtatgtcaaggctgtatgtatcatc 24  
 ||||| | ||||||| ||||| ||||| 466

Db 443 gttgttgcgtgtatgtatcatc 466



xx  
SQ Sequence 249 BP; 58 A; 59 C; 60 G; 72 T; 0 other;  
Query Match 72.5%; Score 17.4; DB 22; Length 249;  
Best Local Similarity 94.7%; Pred. No. 41;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 6 caaggctgtatgacatc 24  
Db 147 caaggctgtatgatcatc 165

RESULT 13  
AAZ40429/C  
ID AAZ40429 standard; DNA; 423 BP.  
XX  
AC AAZ40429;  
XX DT 15-FEB-2000 (first entry)  
Human RAD1 5' EST AA227739.  
XX  
KW Human; RAB1; expressed sequence tag; EST; Schizosaccharomyces pombe; cell cycle checkpoint; genetic alteration; locus; disease; cancer; bladder; head and neck; small cell lung tumour; immune disorder; ss; proliferative disorder; cirrhosis; rheumatoid arthritis; modulator.  
XX OS Homo sapiens.  
XX PN WO200157278-A2.  
XX PD 09-AUG-2001.  
XX PF 30-JAN-2001; 2001WO-US00670.  
XX PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207416.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0265359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488901/53.  
XX PR Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -  
XX PS Claim 25; SEQ ID No 1891; 487pp; English.  
XX DR  
XX CC The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.  
CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/pubseq\\_pct\\_sequences](http://wipo.int/pub/pubseq_pct_sequences).  
XX SQ Sequence 423 BP; 102 A; 107 C; 111 G; 103 T; 0 other;  
Query Match 72.5%; Score 17.4; DB 20; Length 423;  
Best Local Similarity 94.7%; Pred. No. 45;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 6 caaggctgtatgacatc 24  
Db 227 CAAGGCTGTATGATCATC 209

RESULT 14  
AA11958  
ID AA11958 standard; DNA; 474 BP.  
XX AC AA11958;  
XX DT 12-OCT-2001 (first entry)  
DE Probe #1891 for gene expression analysis in human cervical cell sample.  
XX KW Probe; human; microarray; gene expression; cervical epithelial cell; cervical cancer; ss.  
XX OS Homo sapiens.  
XX PN WO200157278-A2.  
XX PD 09-AUG-2001.  
XX PF 30-JAN-2001; 2001WO-US00670.  
XX PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207416.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0265359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488901/53.  
XX PR Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -  
XX PS Claim 25; SEQ ID No 1891; 487pp; English.  
XX DR  
XX CC The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.  
CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/pubseq\\_pct\\_sequences](http://wipo.int/pub/pubseq_pct_sequences).  
XX SQ Sequence 474 BP; 136 A; 91 C; 94 G; 153 T; 0 other;  
Query Match 72.5%; Score 17.4; DB 22; Length 474;  
Best Local Similarity 94.7%; Pred. No. 46;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 6 caaggctgtatgacatc 24  
Db 371 caaggctgtatgatcatc 389

RESULT 15  
AA133289  
ID AA133289 standard; DNA; 474 BP.  
XX AC AA133289;  
XX DT 17-OCT-2001 (first entry)  
XX DE Probe #1975 used to measure gene expression in human placenta sample.

XX  
KW probe; microarray; human; placenta; antenatal diagnosis;  
XX  
KW genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO20015272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00663.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 21-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
(MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488897/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human placenta -  
XX  
PS Claim 25; SEQ ID No 1975; 654pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes (SENP).  
CC The present sequence is one such probe. The probes are useful for  
CC producing a microarray for predicting, measuring and displaying gene  
CC expression in samples derived from human placenta. The probes are useful  
CC for antenatal diagnosis of human genetic disorders.  
XX  
Sequence 474 BP; 136 A; 91 C; 94 G; 153 T; 0 other;  
SQ  

Query	Match	Score	Length
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Db	371 caaggctgtacgtatc	94.7%	389

  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: March 5, 2002, 19:19:05  
Job time: 334.7 sec

Gencore version 4.5.  
Copyright (c) 1993 - 2000 Compugen Ltd.

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	1653	6 AX011208	AX011208 Sequence
C 2	24	100.0	1698	6 AX011206	AX011206 Sequence
C 3	22.4	93.3	1568	6 E33134	E33134 Humanized a
C 4	22.4	93.3	1568	6 D82081	D82081 Mus musculus
C 5	22.4	93.3	1570	5 A77138	A77138 Sequence 6
C 6	22.4	93.3	1570	6 AR029102	AR029102 Sequence
C 7	22.4	93.3	1574	6 AX190434	AX190434 Sequence
C 8	22.4	93.3	1611	6 AX014270	AX014270 Sequence
C 9	19.4	80.8	122680	9 AL133510	AL133510 Human DNA
C 10	19.4	80.8	206773	2 AC010932	AC010932 Homo sapi
C 11	19.2	80.0	71153	9 HUA00662	HUA00662 Homo sapi
C 12	19.2	80.0	977630	9 HUMICRACDV	M44081 Human Tcr-C
C 13	19.2	80.0	175053	2 AC03226	AC03226 Homo sapi
C 14	18.8	78.3	941	2 AC048635	AC048635 Homo sapi
C 15	18.8	78.3	980	2 AC058680	AC058680 Giardia i
C 16	18.8	78.3	1043	2 AC028637	AC028637 Giardia i
C 17	18.8	78.3	1070	2 AC048638	AC048638 Giardia i
C 18	18.8	78.3	1094	2 AC048874	AC048874 Giardia i
C 19	18.8	78.3	101072	9 AC050752	AC050752 Homo sapi
C 20	18.8	78.3	103000	2 AC008727	AC008727 Homo sapi
C 21	18.8	78.3	169897	9 AL353674	AL353674 Human DNA
C 22	18.8	78.3	176788	2 AC021877	AC021877 Homo sapi
C 23	18.8	78.3	181576	2 AC055832	AC055832 Homo sapi
C 24	18.8	78.3	206191	2 AL259642	AL259642 Homo sapi
C 25	18.8	78.3	258654	2 AC008579	AC008579 Homo sapi
C 26	18.4	76.7	1002	2 AC053272	AC053272 Giardia i
C 27	18.4	76.7	89323	9 AP002221	AP002221 Homo sapi
C 28	18.4	76.7	100000	9 AP000084	AP000084 Homo sapi
C 29	18.4	76.7	100000	9 AP000136	AP000136 Homo sapi
C 30	18.4	76.7	171263	2 AE008243	AE008243 Homo sapi
C 31	18.4	76.7	340000	9 AP001693	AP001693 Homo sapi
C 32	18.2	75.8	740	6 AB6287	AB6287 Sequence 94
C 33	18.2	75.8	740	6 AR155780	AR155780 Sequence
C 34	18.2	75.8	740	6 E66305	E66305 Genome DNA
C 35	18.2	75.8	3577	10 MUSTI227A	B50523 Mouse mRNA
C 36	18.2	75.8	11712	1 AE000857	AE000857 Methanobea
C 37	18.2	75.8	25660	9 AL133460	AL133460 Human DNA
C 38	18.2	75.8	94146	9 AC016604	AC016604 Homo sapi
C 39	18.2	75.8	118402	2 AC026629	AC026629 Homo sapi
C 40	18.2	75.8	122458	2 AC010391	AC010391 Homo sapi
C 41	18.2	75.8	154698	2 AC026574	AC026574 Homo sapi
C 42	18.2	75.8	157159	2 AC026279	AC026279 Homo sapi
C 43	18.2	75.8	161345	2 AC091968	AC091968 Homo sapi
C 44	18.2	75.8	162080	2 AC073872	AC073872 Homo sapi
C 45	18.2	75.8	163516	9 AC016635	AC016635 Homo sapi

## ALIGNMENTS

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AX011208/C	1	AX011208	1653 bp	DNA	
DEFINITION		Sequence 3 from Patent	WO957150.		
ACCESSION		AX011208			
VERSION		AX011208.1	GI:9997788		
SOURCE		unidentified	unclassified		
ORGANISM		Kipriyanov,S. and Little,M.	1 (bases 1 to 1653)		
REFERENCE		Kipriyanov,S. and Little,M.	Multivalent antibody constructs		
AUTHORS			Patent: WO 957150-A 3 11-NOV-1999;		
TITLE			DEUTSCHES KREBSFORSCH (DE); KIPRIYANOV SERGEJ (DE); LITTLE MELVYN		
JOURNAL			DEUTSCHES KREBSFORSCH (DE)		
FEATURES			Location/Qualifiers		
SOURCE			/organism="unidentified"		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CDS

28 . 1647  
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SGSGCTDFNLTNPKEVDAITYHQQSTDTPWFGGGKLRKRAADAAAGGGGSQVO  
D82081.1 GR:1565185

VERSION

D82081

OKT3 heavy chain variable region.

SOURCE

MUS musculus hybridoma cell\_line:anti-CD3 monoclonal antibody OKT3

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 418)

Arakawa,F.

DIRECT SUBMISSION

SUBMITTED (20-DEC-1995)

TO THE DDBJ/EMBL/GenBank DATABASES.

Funiko

JOURNAL

Akurawa, School of Medicine, Fukuoka University, First Department

of Biochemistry; 7-451 Nakakuma, Jonan-ku, Fukuoka, Fukuoka

81-4-80, Japan (E-mail:farakawa@msat.fukuoka-u.ac.jp),

2 (bases 1 to 418)

Arakawa,F., Kuroki,M., Kuwahara,M., Senba,T., Ozaki,H.,

Matsuoka,Y., Misumi,Y., Kanda,H. and Watanabe,T.

Cloning and sequencing of the VH and V kappa genes of an anti-CD3..

monoclonal antibody, and construction of a mouse/human chimeric

antibody

J. Biomed. 120 (3), 657-662 (1996)

MEDLINE

97058313

LOCATION/QUALIFIERS

1. loc:418

/organism="Mus musculus"

/cell\_line="anti-CD3 monoclonal antibody OKT3"

/cell\_type="hybridoma"

1. :33

4. :417

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/translation="MDWWTLLFLSVAGVHSQVOLQSGAELARPGASVVKMSCAS

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LAVSLGORATISCKASOVDYEDSYLWVQIOPGGPKLTDASNLVSGIPPRFSC

SGSGCTDFNLTNPKEVDAITYHQQSTDTPWFGGGKLRKRAADAAAGGGGSQVO

D82081

OKT3 heavy chain variable region.

SOURCE

MUS musculus

cDNA to mRNA.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 418)

Arakawa,F.

REFERENCE

1 (bases 1 to 1568)

REFERENCE

1

AUTHORS	Adia, J R A. and Singu, E.J.S. S.	KEYWORDS	
TITLE	Humanized antibody	SOURCE	Unknown.
JOURNAL	Theratech Inc	ORGANISM	Unclassified.
COMMENT	Patent: JP 1999243955-A 4 14-SEP-1999;	REFERENCE	1. (bases 1 to 1570)
OS	Unidentified	AUTHORS	Adair,J.Robert, Athwal,D.Singh and Emtage,J.Spencer.
PN	JP 1999243955-A/4	JOURNAL	Humanised antibodies
PD	14-SEP-1999	FEATURES	Patent: US 5859205-A 6 12-JAN-1999;
PR	22-DEC-1997 JP 1997353861	source	Location/Qualifiers
PI	21-DEC-1989 GB 8928874 0	1. .1570	
C12N15/09, A61K39/395, C07K16/46, C12N5/10//C12P21/08, (C12P21/08, PC	PI	/organism="unidentified"	
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CC	CC		
CC	Strandedness: Single;		
FT	Topology: Linear;		
FH	Location/Qualifiers		
FT	Key		
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ORIGIN	10 others		
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ACCESSION	Sequence 6 from Patent EP0620276.	ACCESSION	AX190434
VERSION	A77138	VERSION	AX190434.1 GI:15143792
KEYWORDS	gtatcgaaaggctataatgatcatc 24	KEYWORDS	
SOURCE	unclassified.	SOURCE	synthetic construct.
ORGANISM	unclassified.	ORGANISM	synthetic construct.
REFERENCE	1 (bases 1 to 1570)	REFERENCE	artificial sequence.
AUTHORS	Adair,J.R. and Emtage,J.S.	AUTHORS	Mueller-Hermelink,H.K., Greiner,A., Doerken,B., Bargou,R. and Kufner,P.
TITLE	HUMANISED ANTIBODIES	TITLE	Antibodies against plasma cells
FEATURES	CELLTECH LTD (GB) Location/Qualifiers	FEATURES	Patent: WO 0147953-A 21-05-JUL-2001;
source	1. .1570	source	Mueller-Hermelink, Hans Konrad (DE) ; Greiner, Axel (DE)
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ACCESSION	Best Local Similarity 95.8%; Pred. No. 3.6; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
RESULT	6	RESULT	8
LOCUS	AR029102/C	LOCUS	AX014270
DEFINITION	1570 bp DNA	DEFINITION	1611 bp DNA
ACCESSION	Sequence 6 from patent US 5859205.	ACCESSION	Sequence 9 from Patent WO9954440.
VERSION	AR029102	VERSION	AX014270
KEYWORDS		KEYWORDS	AX014270.1 GI:10040645
SOURCE		SOURCE	
ORGANISM	human.	ORGANISM	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE	1 (bases 1 to 1611)
AUTHORS	Bargou R., Kufner P., Loeffler A. and Lutterbuese R.	AUTHORS	
TITLE	Cd19xcl3 specific polypeptides and uses thereof	TITLE	
JOURNAL	Patent: WO 9954440-A 9 28-OCT-1999;	JOURNAL	
PAT	29-SEP-1999	PAT	07-SEP-2000

Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>. RP3-481C9 is from the library RPCI-3 constructed by the group of Pliest de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

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repeat_region          14810..15003 /note="MIR repeat: matches 20. .214 of consensus"
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repeat_region          18574..18731 /note="MER2A repeat: matches 1. .161 of consensus"
repeat_region          18737..19048 /note="AlusX repeat: matches 1. .312 of consensus"
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repeat_region          28823..29124 /note="AlusG repeat: matches 1. .303 of consensus"
repeat_region          29175..29444 /note="AlusX repeat: matches 1. .301 of consensus"
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repeat_region          30348..30440 /note="Alus repeat: matches 2. .97 of consensus"
repeat_region          30978..31295 /note="AlusX repeat: matches 1. .312 of consensus"
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repeat_region          33312..33934 /note="L1MC repeat: matches 755. .1410 of consensus"
repeat_region          34198..34625 /note="LTR1 repeat: matches 61. .494 of consensus"
repeat_region          34659..35133 /note="L1MC repeat: matches 1449. .1933 of consensus"
repeat_region          35143..35332 /note="MER2 repeat: matches 6. .95 of consensus"
repeat_region          35233..35584 /note="L1R24 repeat: matches 124. .489 of consensus"
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		KEYWORDS			
		SOURCE			
		ORGANISM			
		Homo sapiens			
		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
		REFERENCE			
		1 (bases 1 to 206773)			
		REFERENCES			
		Birren,B., Linton,L., Nusbaum,C. and Lander,E.			
		AUTHORS			
		Homo sapiens chromosome 15, clone RP11-296E22			
		TITLE			
		Unpublished			
		JOURNAL			
		2 (bases 1 to 206773)			
		REFERENCE			
		Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhglter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearlano,K., Dernon,M., Donegan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Gallegan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.J.C., Johnson,R., Jones,C., Kahn,L., Karatas,A., Klein,J., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKeown,K., McLoughlin,J., Meldrim,J., Morrow,J., Naytor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Polara,V., Riley,R., Roy,A., Santos,R., Severy,P., Starge-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.			
		AUTHORS			
		JOURNAL			
		Submitted (28-SEP-1999) Whitehead Institute/MIT Center for Genome Research			
		On May 25, 2000 this sequence version replaced g1:6479157.			
		All repeats were identified using RepeatMasker:			
		Smit,A.F.A. & Green,P. (1996-1997)			
		<a href="http://ftp.genome.washington.edu/RM/RepeatMasker.html">http://ftp.genome.washington.edu/RM/RepeatMasker.html</a>			
		----- Genome Center			
		Center: Whitehead Institute/MIT Center for Genome Research			
		Center code: WIBR			
		Web site: <a href="http://www-seq.wi.mit.edu">http://www-seq.wi.mit.edu</a>			
		Contact: sequence_submission@genome.wi.mit.edu			
		----- Project Information			
		Center project name: Li634			
		Center clone name: 296_E_22			

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 36 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

FEATURES	SOURCE
*	143059 153724: contig of 12666 bp in length
*	155725 155825: gap of 100 bp
*	155825 167976: contig of 12152 bp in length
*	167977 168075: gap of 100 bp
*	168077 186555: contig of 18579 bp in length
*	186556 186755: gap of 100 bp
*	186756 206773: contig of 20018 bp in length
Location/Qualifiers	
1. . 206773	/organism="Homo sapiens"
	/db_xref="taxon:9006"
	/map="15"
	/clone="RP11-296E22"
	/clone_id="RPCI-11 Human Male BAC"
1. . 1375	1. . 1375
*	*
*	3533 3532: gap of 100 bp
*	3533 4614: contig of 1957 bp in length
*	4615 4714: gap of 100 bp
*	4715 6385: contig of 1671 bp in length
*	6386 6485: gap of 100 bp
*	6486 8036: contig of 1551 bp in length
*	8037 8136: gap of 100 bp
*	8137 9676: contig of 1540 bp in length
*	9677 9776: gap of 100 bp
*	9777 12051: contig of 2275 bp in length
*	12052 12151: gap of 100 bp
*	12152 14712: contig of 2561 bp in length
*	14713 14812: gap of 100 bp
*	14813 16605: contig of 1793 bp in length
*	16606 16705: gap of 100 bp
*	16706 18914: contig of 2109 bp in length
*	18915 18914: gap of 100 bp
*	18915 21644: contig of 2730 bp in length
*	21645 21744: gap of 100 bp
*	21745 24509: contig of 2765 bp in length
*	24510 24609: gap of 100 bp
*	24610 27483: contig of 2459 bp in length
*	27484 27583: gap of 100 bp
*	27584 28893: contig of 2310 bp in length
*	29894 29993: gap of 100 bp
*	29994 32964: contig of 2971 bp in length
*	32965 33064: gap of 100 bp
*	33065 33523: contig of 2459 bp in length
*	33524 35623: gap of 100 bp
*	35624 38490: contig of 2867 bp in length
*	38491 38590: gap of 100 bp
*	38591 43185: contig of 4595 bp in length
*	43186 43285: gap of 100 bp
*	43286 47467: contig of 4182 bp in length
*	47468 47567: gap of 100 bp
*	47568 51338: contig of 3771 bp in length
*	51339 51438: gap of 100 bp
*	51439 55273: contig of 3835 bp in length
*	55274 55373: gap of 100 bp
*	55374 58713: contig of 3340 bp in length
*	58714 58813: gap of 100 bp
*	58814 61102: contig of 5289 bp in length
*	61103 64202: gap of 100 bp
*	64203 70250: contig of 6048 bp in length
*	70251 70350: gap of 100 bp
*	70351 76887: contig of 6537 bp in length
*	76888 76987: gap of 100 bp
*	76988 84690: contig of 7703 bp in length
*	84691 84790: gap of 100 bp
*	84791 94048: contig of 9258 bp in length
*	94049 94148: gap of 100 bp
*	94149 101669: contig of 7521 bp in length
*	101670 101769: gap of 100 bp
*	101770 112318: contig of 10549 bp in length
*	112319 112418: gap of 100 bp
*	112419 121916: contig of 9498 bp in length
*	121917 122016: gap of 100 bp
*	122017 130923: contig of 8907 bp in length
*	130924 131023: gap of 100 bp
*	131024 142958: contig of 11935 bp in length
*	142959 143058: gap of 100 bp





CDS /codon\_start=1  
 /protein\_id="AABB6745\_1"  
 /db\_xref="GI:553737"  
 /translation="ANAGGTSTYKLTFGQQTILTVHP"  
 exon 27429..27491 partial  
 /gene="tcr-alpha"  
 /standard\_name="possible J 52 gene segment"  
 /note="putative"  
 <27841..>27905  
 /gene="tcr-alpha"  
 /standard\_name="possible J 51 gene segment"  
 /note="putative"  
 /codon\_start=3  
 /protein\_id="AABB6746\_1"  
 /db\_xref="GI:339250"  
 /translation="KSLYFWSSCPACAGIVGQADST"  
 CDS <28839..>2895  
 /gene="tcr-alpha"  
 /standard\_name="possible J 50 gene segment"  
 /note="putative"  
 /codon\_start=2  
 /protein\_id="AABB6747\_1"  
 /db\_xref="GI:339251"  
 /translation="ENILRQDGIWARDKLISHS"  
 <29734..>29789  
 /gene="tcr-alpha"  
 /standard\_name="possible J 49 gene segment"  
 /note="putative"  
 /codon\_start=2  
 /protein\_id="AABB6748\_1"  
 /db\_xref="GI:553738"  
 /translation="NTGNQFYFGTGTSLIVIP"  
 CDS <30737..>30799  
 /gene="tcr-alpha"  
 /standard\_name="possible J 48 gene segment"  
 /note="putative"  
 /codon\_start=3  
 /protein\_id="AABB6749\_1"  
 /db\_xref="GI:553739"  
 /translation="SNFGNEKLTFGTGIRLTIPIP"  
 CDS <33096..>33152  
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 /standard\_name="possible J 47 gene segment"  
 /note="putative"  
 /codon\_start=2  
 /protein\_id="AABB6750\_1"  
 /db\_xref="GI:339254"  
 /translation="GINKQQTGLWRRRNHSESQLV"  
 CDS <33647..>33709  
 /gene="tcr-alpha"  
 /standard\_name="possible J 46 gene segment"  
 /note="putative"  
 /codon\_start=3  
 /protein\_id="AABB6751\_1"  
 /db\_xref="GI:553740"  
 /translation="KKSSGDKLTFFGTGTRLAVERP"  
 CDS <34168..>34234  
 /gene="tcr-alpha"  
 /standard\_name="possible J 45 gene segment"  
 /note="putative"  
 /codon\_start=1  
 /protein\_id="AABB6752\_1"  
 /db\_xref="GI:553741"  
 /translation="VYSGGGADGDLTFKGKGTHLLIQP"  
 CDS <35064..>35126  
 /gene="tcr-alpha"  
 /standard\_name="possible J 44 gene segment"  
 /note="putative"  
 /codon\_start=3  
 /protein\_id="AABB6753\_1"  
 /db\_xref="GI:553742"  
 /translation="NTGIAKSLTFFGTGTRLOVTL"  
 CDS  
 COMMENT On Mar 3, 2000 this sequence version replaced gi:7139832.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RW/RepeatMasker.html>  
 ----- Genome Center  
 TITLE JOURNAL  
 SUBMITTED (09-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 REVISIONS  
 On Mar 3, 2000 this sequence version replaced gi:7139832.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RW/RepeatMasker.html>  
 ----- Genome Center



AUTHORS Morrison,H.G., McArthur,A.G., Nixon,J., Eakin,N.Q., Kim,U., Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.  
 TITLE Giardia: a model for ancient eukaryotic genome analysis  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 941)  
 AUTHORS Kim,U., Morrison,H.G., McArthur,A.G., Nixon,J., Eakin,N.Q., Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-APR-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA  
 \* NOTE: This record contains 1 individual

COMMENT sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

BASE COUNT 255 a 239 c 227 g 259 t  
 ORIGIN 1..980  
 FEATURES SOURCE /organism="Giardia intestinalis"  
 /strain="WB-C6"  
 /clone="KJ6211"  
 /db\_xref="taxon:5741"

FEATURES SOURCE /organism="Giardia intestinalis"  
 /strain="WB-C6"  
 /clone="KJ1200"  
 /db\_xref="txon:5741"

BASE COUNT 251 a 226 c 221 g 243 t  
 ORIGIN

FEATURES SOURCE /organism="Giardia intestinalis"  
 /strain="WB-C6"  
 /clone="KJ1200"  
 /db\_xref="txon:5741"

BASE COUNT 251 a 226 c 221 g 243 t  
 ORIGIN

Query Match 78.3%; Score 18.8; DB 2; Length 941;  
 Best Local Similarity 90.9%; Pred. No. 1.9e+02; 0; Mismatches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 gtatgtcaaggctgtatgtatca 22  
 Db 259 GTATGTCAGGCTATAAAGATCA 238

RESULT 15  
 AC088680 AC088680 980 bp DNA HTG 06-FEB-2001  
 LOCUS Giardia intestinalis clone KJ6211 strain WB-C6, LOW-PASS SEQUENCE  
 DEFINITION SAMPLING.

ACCESSION AC088680  
 VERSION AC088680.1 GI:12668594  
 FIELDS HTG; HNGS\_PHASE0  
 SOURCE Giardia intestinalis.

ORGANISM Giardia intestinalis.

REFERENCE 1 (bases 1 to 980)  
 AUTHORS Morrison,H.G., McArthur,A.G., Nixon,J., Eakin,N.Q., Kim,U., Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.  
 TITLE Giardia: a model for ancient eukaryotic genome analysis  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 980)  
 AUTHORS Nixon,J., Morrison,H.G., McArthur,A.G., Eakin,N.Q., Kim,U., Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-FEB-2001) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA  
 \* NOTE: This record contains 1 individual

COMMENT sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone

\* will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1 980: contig of 980 bp in length.

1 Location/Qualifiers

1. .941

1 Query Match 78.3%; Score 18.8; DB 2; Length 980;  
 Best Local Similarity 90.9%; Pred. No. 1.9e+02; 0; Mismatches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 gtatgtcaaggctgtatgtatca 22  
 Db 943 GTATGTCAGGCTATAAAGATCA 964

Search completed: March 5, 2002, 19:15:06  
 Job time: 3248 sec

wed Mar 6 05:49:08 2002

us-09-424-705-7.open.rge

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Om nucleic - nucleic search, using sw model

Run on: March 5, 2002, 18:19:58 ; Search time 1530.11 Seconds  
                   (w/o alignments)  
                   168.549 Million cell updates/sec

Title: US-09-424-705-7

Perfect score: 24

Sequence: gtatgtcaaggctgtatgatcatc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%, Listing first 45 summaries

Database : EST:\*

1: em\_estfun:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estom:\*

5: em\_espl:\*

6: em\_lesta:\*

7: em\_estro:\*

8: em\_estov:\*

9: em\_htc:\*

10: gb\_est1:\*

11: gb\_est2:\*

12: gb\_hcc:\*

13: gb\_gss:\*

14: em\_gss\_fun:\*

15: em\_gss\_hum:\*

16: em\_gss\_inv:\*

17: em\_gss\_pln:\*

18: em\_gss\_pro:\*

19: em\_gss\_rnd:\*

20: em\_gss\_vrt:\*

21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
C 1	18.8	78.3	490	AQ121346 HS_3093_B
C 2	18.8	78.3	613	AQ457569 HS_5097_B
C 3	18.8	78.3	614	AL193627 Tetradon
C 4	18.4	76.7	702	AW442262 EST311658
C 5	18.2	75.8	346	B1319816 ie44a10.y
C 6	18.2	75.8	436	B1319646 ie13h1.y
C 7	18.2	75.8	471	BT135180 UI-M-BH3-
C 8	18.2	75.8	477	AQ831679 HS_2099_A
C 9	18.2	75.8	511	AQ713927 HS_2122_B
C 10	18.2	75.8	513	BT13823 UI-M-BH3-
C 11	18.2	75.8	515	BT133300 UI-M-BH3-
C 12	18.2	75.8	550	BE946941 UI-M-BH3-

**RESULTS**

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	AQ121346	490 bp DNA	HS_3083_B	Locus	Plate=3083 Col=19 Row=H	GSS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1	AQ121346	Approved Human Genomic Sperm Library D	HS_3083_B	Definition	Plate=3083 Col=19 Row=H	D	Homo
1	AQ121346	Human	HS_3083_B	Accession	Row=H	...	...
1	AQ121346.1	GI:3498512	HS_3083_B	Version	...	...	...
1		GSS	HS_3083_B	Keywords	...	...	...
1			HS_3083_B	Source	...	...	...
1			HS_3083_B	Organism	...	...	...

**REFERENCE**

1 (bases 1 to 490)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

**AUTHORS**

**TITLE**

Sequencing the human genome: A sequence approach to mapping and scanning the human connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

**JOURNAL**

99380589

**COMMENT**

Contact: Mahairas GG, Wallace JC, Hood L  
                   High Throughput Sequencing Center  
                   University of Washington  
                   401 Queen Anne Avenue North, Seattle, WA 98109, USA  
                   Tel: (206) 616-3619  
                   Fax: (206) 616-3887  
                   Email: jwallace@u.washington.edu

**FEATURES**

Sequence Tagged Connector  
                   Plane: 3083 row: H column: 19  
                   Class: BAC ends  
                   High quality sequence stop: 490.  
                   Location/Qualifiers  
                   1. .490  
                   organism="Homo sapiens"  
                   /db\_xref="taxon:9605"

/clone="Plate=3083 Col=19 Row=H"  
 /clone.lib="CIT Approved Human Genomic Sperm Library D"  
 /sex="male"  
 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in  
 E-Coli DH10B"

BASE COUNT	ORIGIN	RESULT	Matches	Conservative	Mismatches	Indels	Gaps	O;
117	a	1	78.3%	Score 18 8; DB 13;	Length 490;			
	99	1	Best Local Similarity 90.9%;	Pred. No. 2.8e+02;				
	c	1	Matches 20; Conservative	0; Mismatches	2;	Indels	0;	Gaps
	95	1	20; Conservative	0; Mismatches	2;	Indels	0;	Gaps
	9	1	2; Indels	0;	2;	Indels	0;	Gaps
141	a	1	90.9%; Score 18 8; DB 13;	Length 613;				
142	c	1	Best Local Similarity 90.9%;	Pred. No. 2.9e+02;				
	107	1	21 others					

Query Match 78.3%; Score 18 8; DB 13; Length 490;  
 Best Local Similarity 90.9%; Pred. No. 2.8e+02; Length 614;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtatgtcaaggcttaatgtatca 22  
 Db 424 GTAGTCAGGCTCAATGAGCA 343

RESULT 2  
 BASE COUNT 67569/c  
 DEFINITION HS\_5097\_B1\_D07\_T7A RCI-11 Human Male BAC Library Homo sapiens  
 ACCESSION A0457569  
 VERSION A0457569.1 GI:4636209  
 KEYWORDS GSS.  
 SOURCE homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buterilia; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 613)  
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Smartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
 COMMENT High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm)) or from Research Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC end Web Server: <http://www.htsc.washington.edu>  
 Plate: 673 row: H column: 13  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 613.  
 FEATURES source  
 1. .613  
 /organism="homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate=673 Col=13 Row=H"  
 /clone.lib="RPCI-11 Human Male BAC Library"  
 /sex="male"  
 /note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylyase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"  
 BASE COUNT 154 a  
 ORIGIN RESULT 3  
 CNS02EEA CNS02EEA 614 bp DNA GSS 13-MAY-2000  
 DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 262017 of library G from Tetraodon nigroviridis, genomic survey sequence.  
 ACCESION AI193627  
 VERSION AI193627.1 GI:7831733  
 KEYWORDS GSS; genome survey sequence.  
 SOURCE Tetraodon nigroviridis  
 ORGANISM Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontidae; Tetraodon.  
 REFERENCE 1 (bases 1 to 614)  
 AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
 TITLE JOURNAL Unpublished  
 JOURNAL, Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizians,C., Winkler,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
 TITLE Unpublished  
 JOURNAL, Human gene number estimate provided by genome wide analysis using tetraodon nigroviridis DNA sequence  
 JOURNAL, Unpublished  
 REFERENCE 3 (bases 1 to 614)  
 AUTHORS Genoscope.  
 TITLE JOURNAL Direct Submission  
 COMMENT Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, Please take a look at <http://www.genoscope.cnrs.fr/Tetraodon>.  
 FEATURES source  
 1. .614  
 /organism="Tetraodon nigroviridis"  
 /db\_xref="taxon:99883"  
 /clone="262017"  
 /clone.lib="G"  
 /note="Genoscope sequence ID : COAG262AH09SP1-end : PUC-Ori",  
 BASE COUNT 164 a  
 ORIGIN RESULT 4  
 AW442262/C AW442262 702 bp mRNA EST 18-MAY-2001  
 LOCUS EST311658 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA  
 DEFINITION clone CLLEN2110 5', mRNA sequence.  
 ACCESSION AW442262  
 VERSION AW442262.1 GI:6977513  
 KEYWORDS EST.

Gencore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: March 5, 2002, 18:22:38 ; Search time 67.11 Seconds

(without alignments)  
80.993 Million cell updates/sec

Title: US-09-424-705-7

Perfect score: 24

Sequence: 1 gragtcaaggctgtatgatcatc 24

Scoring table: IDENTITY\_NUC

GapOp 10.0 , capext 1.0

Searched: 351203 seqs, 113238999 residues

The number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptdatadna/lina/5B\_COMBO.seq: \*  
2: /cgn2\_6/ptodata/lina/5B\_COMBO.seq: \*  
3: /cgn2\_6/ptodata/lina/6A\_COMBO.seq: \*  
4: /cgn2\_6/ptodata/lina/6B\_COMBO.seq: \*  
5: /cgn2\_6/ptodata/lina/PCTUS\_COMBO.seq: \*  
6: /cgn2\_6/ptodata/lina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	ALIGNMENTS
C 1	23.4	93.3	1570	2 US-08-303-569B-6	Sequence 6, Appli	Sequence 6, Appli
C 2	22.4	93.3	1570	2 US-08-16-247-6	Sequence 6, Appli	Sequence 1, Appli
C 3	18.2	75.8	740	4 US-08-990-416-946	Sequence 946, Appli	Sequence 40, Appli
C 5	16.6	69.2	2297	2 US-08-800-644-110	Sequence 110, Appli	Sequence 41, Appli
C 6	16.6	66.7	227	4 US-08-991-789-183	Sequence 183, Appli	Sequence 4, Appli
C 7	16.6	77.3	4	US-08-988-416-569	Sequence 569, Appli	Sequence 4, Appli
C 8	16.6	1041	2	US-08-613-2205-3	Sequence 3, Appli	Sequence 4, Appli
C 9	16.6	66.7	2399	2 US-08-070-116-1	Sequence 1, Appli	Sequence 31, Appli
C 10	16.6	66.7	2635	1 US-08-253-685-1	Sequence 1, Appli	Sequence 40, Appli
C 11	15.6	65.0	830	4 US-08-387-707-13	Sequence 13, Appli	Sequence 41, Appli
C 12	15.6	65.0	1610	3 US-08-889-108-7	Sequence 7, Appli	Sequence 4, Appli
C 13	15.6	65.0	5	PCN-94-10350-7	Sequence 2, Appli	Sequence 4, Appli
C 14	15.6	65.0	2038	2 US-08-730-770-2	Sequence 1, Appli	Sequence 4, Appli
C 15	15.6	65.0	2160	4 US-08-180-275A-1	Sequence 17, Appli	Sequence 4, Appli
C 16	15.6	65.0	16373	3 US-09-128-582-1	Sequence 13, Appli	Sequence 4, Appli
C 17	15.2	63.3	630	4 US-09-385-982-89	Sequence 7, Appli	Sequence 4, Appli
C 18	15.2	63.3	1411	3 US-08-878-474-2	Sequence 7, Appli	Sequence 4, Appli
C 19	15.2	63.3	3500	4 US-09-197-636-7	Sequence 21, Appli	Sequence 4, Appli
C 20	15.2	63.3	4164	1 US-08-180-582-3	Sequence 3, Appli	Sequence 4, Appli
C 21	15.2	63.3	4164	1 US-08-646-715-3	Sequence 3, Appli	Sequence 4, Appli
C 22	15.2	63.3	4803	4 US-09-197-636-3	Sequence 3, Appli	Sequence 4, Appli
C 23	15.2	63.3	4803	4 US-09-197-636-3	Sequence 20, Appli	Sequence 4, Appli
C 24	15.2	63.3	246240	2 US-08-724-394A-20	Sequence 21, Appli	Sequence 4, Appli
C 25	15.2	63.3	246240	2 US-08-724-394A-22	Sequence 22, Appli	Sequence 4, Appli
C 26	15.2	63.3	246240	2 US-08-724-394A-22	Sequence 1, Appli	Sequence 4, Appli
C 27	15.2	63.3	4411529	4 US-09-103-840A-1	Query Match	Sequence 1, Appli

RESULT 2  
 US-08-116-247-6/c  
 ; Sequence 6, Application US/08116247  
 ; Patent No. 5929212

GENERAL INFORMATION:  
 APPLICANT: Jolliffe, Linda K.  
 APPLICANT: Zivin, Robert A.  
 APPLICANT: Adair, John R.  
 APPLICANT: Athwal, Diljeet S.  
 TITLE OF INVENTION: CD3 Specific Recombinant Antibody  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris  
 STREET: One Liberty Place - 46th Floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/116,247  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/7743,377  
 FILING DATE: 10-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Paintin, Francis A.  
 REGISTRATION NUMBER: 19,386  
 REFERENCE/DOCKET NUMBER: CARP-0011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3439  
 TELEFAX: (215) 568-3100  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1570 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 NAME/KEY: CDS  
 LOCATION: 41..1444  
 US-08-116-247-6

RESULT 3  
 Query Match 93.3%; Score 22.4; DB 2; Length 1570;  
 Best Local Similarity 95.8%; Pred No. 0.027; 1; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gtatcaaggctgtatgtatc 24  
 Db 421 GTAGTCAAGGCACTAATGATCATC 398

GENERAL INFORMATION:  
 APPLICANT: Philipsen, Peter  
 APPLICANT: Pohlmann, Rainer

RESULT 4  
 US-08-056-200-110/c  
 ; Sequence 110, Application US/08056200  
 ; Patent No. 5616500  
 ; GENERAL INFORMATION:  
 APPLICANT: Steinert, Peter M.  
 APPLICANT: Lee, Seung-Chul  
 APPLICANT: Kim, In-Gyu  
 APPLICANT: Chung, Soo-II  
 APPLICANT: Park, Sang-Chul  
 TITLE OF INVENTION: Trichomyalin and Transglutaminase-3 and  
 NUMBER OF SEQUENCES: 117  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive, Sixteenth Floor  
 CITY: Newport Beach  
 STATE: CA

RESULT 5  
 Query Match 75.8%; Score 18.2; DB 4; Length 740;  
 Best Local Similarity 87.0%; Pred No. 2.8; 3; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gtatcaaggctgtatgtatc 23  
 Db 172 GTAGTCAAGGCACTGTTAT 150

GENERAL INFORMATION:  
 APPLICANT: Steinert, Peter M.  
 APPLICANT: Lee, Seung-Chul  
 APPLICANT: Kim, In-Gyu  
 APPLICANT: Chung, Soo-II  
 APPLICANT: Park, Sang-Chul  
 TITLE OF INVENTION: Methods of Using Same  
 NUMBER OF SEQUENCES: 117  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive, Sixteenth Floor  
 CITY: Newport Beach  
 STATE: CA

APPLICANT: Steiner, Sabine  
 APPLICANT: Mohr, Christine  
 APPLICANT: Wendland, Jurgen  
 APPLICANT: Knechtle, Philipp  
 APPLICANT: Reischlburg, Corinne  
 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII  
 NUMBER OF SEQUENCES: 1152  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 623926artis Corporation  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: NC 27709 USA  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/998,416  
 FILING DATE: 24-DEC-1997  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: CH 0016/97  
 FILING DATE: 31-DEC-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-541-8887  
 TELEFAX: 919-541-8689  
 INFORMATION FOR SEQ ID NO: 946:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 740 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 ORGANISM: PAG1585UP  
 ; US-08-998-416-946

RESULT 6  
 Query Match 93.3%; Score 22.4; DB 2; Length 1570;  
 Best Local Similarity 95.8%; Pred No. 0.027; 1; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gtatcaaggctgtatgtatc 23  
 Db 172 GTAGTCAAGGCACTGTTAT 150

GENERAL INFORMATION:  
 APPLICANT: Steinert, Peter M.  
 APPLICANT: Lee, Seung-Chul  
 APPLICANT: Kim, In-Gyu  
 APPLICANT: Chung, Soo-II  
 APPLICANT: Park, Sang-Chul  
 TITLE OF INVENTION: Trichomyalin and Transglutaminase-3 and  
 NUMBER OF SEQUENCES: 117  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive, Sixteenth Floor  
 CITY: Newport Beach  
 STATE: CA

APPLICANT: Steiner, Sabine  
 APPLICANT: Mohr, Christine  
 APPLICANT: Wendland, Jurgen  
 APPLICANT: Knechtle, Philipp  
 APPLICANT: Reischlburg, Corinne  
 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII  
 NUMBER OF SEQUENCES: 1152  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 623926artis Corporation  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: NC 27709 USA  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/998,416  
 FILING DATE: 24-DEC-1997  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: CH 0016/97  
 FILING DATE: 31-DEC-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-541-8887  
 TELEFAX: 919-541-8689  
 INFORMATION FOR SEQ ID NO: 946:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 740 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 ORGANISM: PAG1585UP  
 ; US-08-998-416-946

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OM nucleic - nucleic search, using sw model  
Run on: March 5, 2002, 19:15:08 ; Search time 1556.36 Seconds  
(without alignments)  
254.396 Million cell updates/sec

Title: US-09-424-705-7

Perfect score: 24  
Sequence: 1 gtatgttcaaggctgttatgtatcatc 24

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Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Number of hits satisfying chosen parameters: 309068

Minimum DB seq length: 0  
Maximum DB seq length: 24

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

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c	3	13.2	55.0	21	6	AX015842	AX015842 Sequence
c	4	13.2	55.0	23	6	AX146761	AX146761 Sequence
c	5	12.8	53.3	19	6	E05167	E05167 Oligonucleo
c	6	12.6	52.5	24	6	AR153077	AR153077 Sequence
c	7	12.4	51.7	21	6	AX095872	AX095872 Sequence
c	8	12.2	50.8	20	6	AX089242	AX089242 Sequence
c	9	12.2	50.8	23	6	AX183705	AX183705 Sequence
c	10	12.2	50.8	23	6	I20550	I20550 Sequence 5
c	11	12.2	50.8	23	6	I20565	I20565 Sequence 24
c	12	12.2	50.8	24	6	AX147428	AX147428 Sequence
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c	14	12	50.0	21	6	A63960	A63960 Sequence 4
c	15	12	50.0	21	6	AR091470	AR091470 Sequence
c	16	11.8	49.2	17	6	AX029248	AX029248 Sequence
c	17	11.8	49.2	18	6	I78198	I78198 Sequence 90
c	18	11.8	49.2	20	6	AX0419	AX04199 Sequence
c	19	11.8	49.2	24	6	AX116463	AX116463 Sequence
c	20	11.6	48.3	18	6	AR151248	AR151248 Sequence
c	21	11.6	48.3	20	6	A44370	A44370 Sequence 18
c	22	11.6	48.3	20	6	AR03733	AR03733 Sequence
c	23	11.6	48.3	20	6	AR127296	AR127296 Sequence
c	24	11.6	48.3	20	6	I95598	I95598 Sequence 26
c	25	11.6	48.3	24	6	AX022974	AX022974 Sequence
c	26	11.6	48.3	24	6	AX031224	AX031224 Sequence
c	27	11.4	47.5	21	6	AX117243	AX117243 Sequence
c	28	11.2	46.7	17	6	AR037574	AR037574 Sequence
c	29	11.2	46.7	17	6	AR15326	AR15326 Sequence
c	30	11.2	46.7	19	6	AR137256	AR137256 Sequence
c	31	11.2	46.7	19	6	AR156526	AR156526 Sequence
c	32	11.2	46.7	19	6	AX037378	AX037378 Sequence
c	33	11.2	46.7	20	6	A67865	A67865 Sequence 37
c	34	11.2	46.7	20	6	AR051717	AR051717 Sequence
c	35	11.2	46.7	20	6	AR051719	AR051719 Sequence
c	36	11.2	46.7	20	6	AR067707	AR067707 Sequence
c	37	11.2	46.7	20	6	AR118894	AR118894 Sequence
c	38	11.2	46.7	20	6	I18250	I18250 Sequence 34
c	39	11.2	46.7	20	6	I18252	I18252 Sequence 36 ..
c	40	11.2	46.7	21	6	AR016125	AR016125 Sequence
c	41	11.2	46.7	21	6	AR019123	AR019123 Sequence
c	42	11.2	46.7	21	12	AB068356	AB068356 Synthetic
c	43	11.2	46.7	22	6	AR139330	AR139330 Sequence
c	44	11.2	46.7	22	6	AX18195	AX18195 Sequence 117576 Sequence 9
c	45	11.2	46.7	22	6	I17576	I17576 Sequence 9

## ALIGNMENTS

RESULT 1  
AX099949/c  
LOCUS AX099949  
DEFINITION Sequence 9 from Patent WO0120034.  
ACCESSION AX099949  
VERSION 1  
KEYWORDS

SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 17)  
Voss,J. and Timm,J.  
AUTHORS Methods and compositions for the screening of cell cycle modulators  
TITLE Patent: WO 0120034-A 9-22-MAR-2001;  
JOURNAL BASF AKTIENGESELLSCHAFT (DE)  
FEATURES Location/Qualifiers

source  
organism="Mus musculus"  
/ab\_xref="Taxon:10090"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



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Om nucleic - nucleic search, using sw model

Run on: March 5, 2002, 19:16:13 ; Search time 1481.91 Seconds

(without alignments)  
174.031 Million cell updates/sec

Title: US-09-424-705-7

perfect score: 24  
Sequence: 1 gtagtcaaggctgtatgatcatc 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 13210

Minimum DB seq length: 0

Maximum DB seq length: 24

post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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4: em\_estpl:\*

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7: em\_estov:\*

8: em\_htc:\*

9: em\_htc1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_gss:\*

13: em\_gss\_fun:\*

14: em\_gss\_hum:\*

15: em\_gss\_inv:\*

16: em\_gss\_plh:\*

17: em\_gss\_pro:\*

18: em\_gss\_rdt:\*

19: em\_gss\_vrt:\*

20: em\_gss\_other:\*

#### SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### ALIGNMENTS

RESULT 1  
AV833359/c

DEFINITION AZ833359 22 bp DNA  
LOCUS clone UGGC2M0115G19 F, DNA sequence.

ACCESSION AZ833359  
VERSION AZ833359.1 GI:1303267  
KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

DEFINITION AZ833359 22 bp DNA  
LOCUS clone UGGC2M0115G19 F, DNA sequence.

ACCESSION AZ833359  
VERSION AZ833359.1 GI:1303267  
KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Peiersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
Tel: 801 585 5006  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00  
Plate: 0115 Row: G column: 19  
Seq primer: CGGTTGAAACGGACGCCAGT

Class: Plasmid ends

High quality sequence stop: 22.  
Location/Qualifiers 1. .22

FEATURES source  
1. .22

source

1.	.24	/organism="Mus musculus"	
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		/db_xref="txon:10090"	
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		/clone=211d02"	
		/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"	
		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://www.Jax.org/resources/documents/dnares/">http://www.Jax.org/resources/documents/dnares/</a> ). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 Polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g914732114 gb AF129072.1), a copy-number inducible derivative of plasmid pRL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
BASE COUNT	3 a 8 a	8 c 1 g	5 t 5 t
ORIGIN			

Query Match

QY	3	agtcaaggctgtatgtatcc	24
Db	24	AGTANAGGGAGATAGACCC	3

RESULT

RESULT	3		
AZCU	A2507472/C	19 bp	DNA
DEFINITION	IM0349D11F	Mouse 10kb plasmid UUGCIM library	Mus musculus genomic clone UUGCIM0349D11 F, DNA sequence.
ACCESSION	A2507472		
VERSION	A2507472.1	GI:10688788	
KEYWORDS	GSS, house mouse.		
ORGANISM	Mus musculus		

REFERENCE

REFERENCE	1	(bases 1 to 19)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly.., M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.		
TITLE	Plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss		

JOURNAL

UNPUBLISHED	2000		
CONTACT	Robert B. Weiss		

COMMENT

UNPUBLISHED	2000		
CONTACT	Robert B. Weiss		

FEATURES

SOURCE	1.19		
		/organism="Mus musculus"	
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		/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"	
		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://www.Jax.org/resources/documents/dnares/">http://www.Jax.org/resources/documents/dnares/</a> ). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 Polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g914732114 gb AF129072.1), a copy-number	

FEATURES

LOCATION/QUALIFIERS	High quality sequence stop: 19.		
QUALIFIERS	Location/Qualifiers		

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## OM nucleic - nucleic search, using sw model

Run on: March 5, 2002, 20:07:18 ; Search time 168.74 Seconds

(without alignments)  
(121.938 Million cell updates/sec)

Title: US-09-424-705-7  
Perfect score: 24  
Sequence: 1 gtagtcaaggctgtatgatcatc 24  
Scoring table: IDENTITY\_NUC  
GapOp 10.0 , Gapext 1.0

Searched: 930621 seqs, 428656219 residues

Number of hits satisfying chosen parameters: 607738

Minimum DB seq length: 0

Maximum DB seq length: 24

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_1101:\*

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21: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT:\*

22: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	24	100.0	24 19 AAV7336	Mouse OKT3 variant
2	15	62.5	17 22 AAF57365	Murine Cdc25A intr Probe DI_3CR3A fo
3	13.8	57.5	24 13 AAQ23468	Probe DI_3CR3A fo
4	13.6	56.7	24 15 AAQ01088	Mutagenic primer f
5	13.2	55.0	21 20 AAZ2535	Human retrovirus-5
6	13.2	55.0	22 19 AAV49973	PCR primer for hum
7	13.2	55.0	21 AAX82713	Human IgA nephropo
8	13.2	53.0	23 22 AAD05820	Human vanilloid re
9	12.8	53.3	19 14 AAO61590	Campylobacter bact
10	12.8	53.3	21 22 AAF56285	Human gene singl
11	12.8	53.3	24 19 AAV49937	PCR primer for hum

## ALIGNMENTS

RESULT 1	AAV7336	ID AA7336 standard; DNA; 24 BP.
	XX	AC AA7336;
	XX	DT 26-FEB-1999 (first entry)
	XX	DE Mouse OKT3 variant antibody primer SKI DNA.
	XX	KW OKT3; monoclonal antibody; Mab; point mutation; transplant rejection; organ recipient; diagnosis; tumour; therapy; primer; ss.
	XX	OS Synthetic.
	OS	Mus sp.
	XX	PN DE19721700-C1.
	XX	PD 19-NOV-1998.
	XX	PF 23-MAY-1997; 97DE-1021700.
	PR XX	23-MAY-1997; 97DE-1021700.
	PA XX	(DEKR-) DEUT KREISFORSCHUNGSZENTRUM.
	PI XX	Kirriyanov S, Little M, Moldenhauer G;
	XX	DR WPI; 1998-596150/51.
	PT XX	Monoclonal antibody OKT3 with point-mutation - where cysteine is replaced by another polar amino acid, useful for controlling transplant rejection, and in tumour diagnostics and therapy
	PT XX	PT

PS	claim 7; Column 3; 8pp; German.
CC	This sequence is a primer used in the construction of a monoclonal antibody (Mab) derived from OK3 with a point-mutation where Cys at position H100A is replaced with another polar amino acid, in this example Ser. The Mab is used in lowering or eliminating the transplant rejection in an organ recipient and for diagnostic methods for tumours and tumour therapy.
CC	Sequence 24 BP; 7 A; 4 C; 6 G; 7 T; 0 other;
CC	XX
SQ	Query Match 100.0%; Score 24; DB 19; Length 24; Best Local Similarity 100.0%; Pred. No. 0.019; Mismatches 0; Matches 24; Conservative 0; Indels 0; Gaps 0;
QY	1 gtagtcagaaggctgtatgtatcatc 24
DN	1 gtatgcagaaggctgtatgtatcatc 24
RESULT	2
ID	RAF5/365/C
XX	RAF5/365 standard; DNA; 17 BP.
AC	RAF5/365;
XX	RAF5/365;
DT	11-JUN-2001 (first entry)
DE	Murine Cdc25A intron 3/exon 4 splice junction sequence.
XX	Cdc25: Cdc25 phosphatase; transcription; modulator; murine; Cdc25A; exon; intron; ds.
KW	Mus sp.
OS	XX
PN	WO200120034-A2.
XX	PD
XX	22-MAR-2001.
PF	11-SEP-2000; 2000WO-US24838.
PR	13-SEP-1999; 99US-0153639.
XX	(BADI ) BASF AG.
PA	Voss J, Timm J;
PT	WPI; 2001-244825/25.
XX	XX
PT	Assay for screening modulators of Cdc25 activity by using a cell having a recombinant Cdc25 phosphatase gene whose expression alters the transcription of a selected gene in the presence of a modulator -
XX	Example 1; Page 15; 55pp; English.
PS	The invention relates to a method of identifying a modulator of Cdc25 activity that comprises contacting a test cell having a recombinant Cdc25 phosphatase gene whose expression alters transcription of a selected gene, with a compound under conditions where recombinant Cdc25 phosphatase gene is expressed and alters the transcription of a selected gene as an indication of the compound being a modulator of Cdc25-mediated transcription. The method is useful for identifying modulators of Cdc25 activity. Sequences RAF5/365-376 represent intron/exon splice junction sequences of the murine Cdc25A gene.
XX	Sequence 17 BP; 5 A; 5 C; 2 G; 5 T; 0 other;
XX	XX

QY		5	tcaaggcttataatga	19
Db		16		
	RESULT	3		
	ARQ23468			
	ID	AAQ23468	standard; DNA; 24 BP.	
	XX			
	AC	AAQ23468;		
	XX			
	DT	21-MAY-1992	( first entry)	
	XX			
	DE	Probe D1.3CDR3A for pAB D1.3;		
	XX			
	KW	Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;		
	KW	pius; g3p; binding; adsorption; gene VIII; diverse repertoire;		
	KW	specific binding pairs; replicable genetic display package;		
	KW	immunoglobulin; ss.		
	XX			
	OS	Synthetic.		
	XX			
	PN	WO9201047-A.		
	XX			
	PD	23-JAN-1992.		
	XX			
	PF	10-JUL-1991;	91WO-GB01134.	
	XX			
	PR	15-MAY-1991;	91GB-00100549.	
	PR	10-JUL-1990;	90GB-0015198.	
	PR	19-OCT-1990;	90GB-00322845.	
	PR	12-NOV-1990;	90GB-0034503.	
	PR	05-MAR-1991;	91GB-0004744.	
	XX			
	PA	(CAMPB-) CAMBRIDGE ANTIBODY.		
	PA	(MEDL-) MED RES COUNCIL.		
	XX			
	PI	McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;		
	PI	Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;		
	PI	Winter GP, Bonnett TP;		
	XX			
	DR	WPI; 1992-056862/07.		
	XX			
	PT	Producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic display package.		
	XX			
	PS	Example 10; Page 57; 209pp; English.		
	XX			
	CC	The probe was used to distinguish between pAB D1.3 and pAB NQ11 which express antibody fragments specific for hen egg lysozyme and oxazalone respectively. The probe was used to monitor the enrichment of pAB D1.3 from a mixed vector population contg. pAB NQ11 by application to a lysozyme sepharose column. An enrichment of 1000 fold was achieved in one round.		
	CC	See also AAQ21092-100, 103-116, 126-131; AAQ23463, 465-495, 693-719, 736-738, and 793-863.		
	XX			
	SQ	Sequence 24 BP; 6 A; 7 C; 3 G; 8 T; 0 other;		
	Query	Match	57.5%	Score 13.8; DB 13; Length 24;
	best Local Similarity	88.2%	Pred. No. 1.4e+03;	
	Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps	
OY	1	gttagtcacggctgttaat	17	
	1	gttagtcacggccataat	17	

GenCore version 4.5  
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## On nucleic - nucleic search, using sw model

Run on: March 5, 2002, 19:19:13 ; Search time 66.33 Seconds

(without alignments)

81.946 Million cell updates/sec

Title: US-09-424-705-7  
Perfect score: 24  
Sequence: 1 gtaqtcaaggctgtatgatcatc 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 1132238929 residues

T number of hits satisfying chosen parameters: 281400

Minimum DB seq length: 0

Maximum DB seq length: 24

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database : Issued\_Patents\_NA:\*

1: /egn2\_6/podata/1/ina/5A\_COMB.seq: \*  
2: /egn2\_6/podata/1/ina/5B\_COMB.seq: \*  
3: /con2\_6/podata/1/ina/6A\_COMB.seq: \*  
4: /egn2\_6/podata/1/ina/6B\_COMB.seq: \*  
5: /egn2\_6/podata/1/ina/PCITS\_COMB.seq: \*  
6: /con2\_6/podata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	12.6	52.5	24	4	US-09-358-972-78	Sequence 78, Appl
c 2	12.4	51.7	24	5	PCT-US95-10973A-64	Patent No. 623480
c 3	12.2	50.8	23	1	US-07-963-290A-5	GENERAL INFORMATION:
c 4	12.2	50.8	23	1	US-07-963-290A-24	APPLICANT: Shultz, John W
c 5	12.2	50.8	23	3	US-08-819-867-38	APPLICANT: Lewis, Martin K.
c 6	12	50.0	20	2	US-09-289-368-56	APPLICANT: Lieper, Donna
c 7	12	50.0	21	2	US-08-781-620B-4	APPLICANT: Mandrekar, Michelle
c 8	11.8	49.2	18	1	US-08-334-847-905	APPLICANT: Kephart, Daniel
c 9	11.8	49.2	23	3	US-08-819-867-37	APPLICANT: Rhodes, Richard B.
c 10	11.6	48.3	24	3	US-08-760-354A-21	APPLICANT: Andrews, Christine A.
c 11	11.6	48.3	18	4	US-07-861-458C-74	APPLICANT: Hartnett, James R.
c 12	11.6	48.3	20	1	US-08-332-747-26	APPLICANT: Gu, Trent
c 13	11.6	48.3	20	3	US-09-009-913-257	APPLICANT: Olson, Ryan J.
c 14	11.6	48.3	20	4	US-09-429-093-2	APPLICANT: Wood, Keith W.
c 15	11.6	48.3	24	4	US-03-230-804-24	APPLICANT: Welch, Roy
c 16	11.4	47.5	23	1	US-08-753-147-92	APPLICANT: Kephart, Daniel
c 17	11.2	46.7	17	2	US-08-292-620A-1778	APPLICANT: Lewis, Martin K.
c 18	11.2	46.7	17	3	US-08-983-162-187	APPLICANT: Mandrekar, Michelle
c 19	11.2	46.7	17	3	US-09-071-845-1778	APPLICANT: Kephart, Daniel
c 20	11.2	46.7	19	4	US-09-050-159-3	APPLICANT: Rhodes, Richard B.
c 21	11.2	46.7	19	4	US-03-407-818-10	APPLICANT: Andrews, Christine A.
c 22	11.2	46.7	20	1	US-08-342-785-34	APPLICANT: Hartnett, James R.
c 23	11.2	46.7	20	1	US-08-343-785-36	APPLICANT: Gu, Trent
c 24	11.2	46.7	20	2	US-08-463-221-34	APPLICANT: Olson, Ryan J.
c 25	11.2	46.7	20	2	US-08-462-221-36	APPLICANT: Wood, Keith W.
c 26	11.2	46.7	20	2	US-08-447-031A-3	APPLICANT: Welch, Roy
c 27	11.2	46.7	20	3	US-08-946-458-36	APPLICANT: Kephart, Daniel

## ALIGNMENTS

RESULT 1  
US-09-358-972-78/c  
Sequence 78, Application US/09358972  
; Sequence 78, Application US/09358972  
; Patent No. 623480  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Lieper, Donna  
; APPLICANT: Mandrekar, Michelle  
; APPLICANT: Kephart, Daniel  
; APPLICANT: Rhodes, Richard B.  
; APPLICANT: Andrews, Christine A.  
; APPLICANT: Hartnett, James R.  
; APPLICANT: Gu, Trent  
; APPLICANT: Olson, Ryan J.  
; APPLICANT: Wood, Keith W.  
; APPLICANT: Welch, Roy  
; TITLE OF INVENTION: Nucleic Acid Detection  
; FILE REFERENCE: Pro-103 6868/75528  
; CURRENT APPLICATION NUMBER: US-09/358, 972  
; EARLIER APPLICATION NUMBER: 09/252, 436  
; EARLIER FILING DATE: 1999-02-18  
; EARLIER APPLICATION NUMBER: 09/042, 287  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO: 78  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Upstream probe for kanamycin  
; QUERY Match  
; Best Local Similarity 52.5%; Score 12.6%; DB 4;  
; Matches 15; Conservative 0; Mismatches 4;  
; Indels 0; Gaps 0;  
; QY 4 gtcagaggctgtatgatca 22  
; Db 19 GTCAAGACTCTTACGATCA 1  
; RESULT 2  
; PCT-US95-10973A-64/c  
; Sequence 64, Application PC/TUS9510973A  
; GENERAL INFORMATION:  
; APPLICANT: Prism Pharmaceuticals, Inc.  
; TITLE OF INVENTION: CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGE  
; NUMBER OF SEQUENCES: 107

## CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BARRY  
 STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle  
 STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10973A

FILING DATE: 29-AUG-1995

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Notterberg, Carol

REGISTRATION NUMBER: 39,317

REFERENCE/DOCKET NUMBER: 760100.413PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 622-6031

## INFORMATION FOR SEQ ID NO: 64:

## SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT-US95-10973A-64

Query Match 51.7%; Score 12.4; DB 5; Length 24;  
 Best Local Similarity 72.7%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 agtcaggctgtatgatc 24  
 Db 23 AGCCGAGGGGTGAGGATC 2

RESULT 3

US-07-963-290A-5

; Sequence 5, Application US/07963290A

; Patent No. 5514586

## GENERAL INFORMATION:

APPLICANT: HOTTINGER, Herbert

APPLICANT: NIEDERBERGER, Peter

APPLICANT: PRIDMORE, David

APPLICANT: STRAEGER, Ursula

TITLE OF INVENTION: FOOD ADDITIVES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: VOGT & O'DONNELL

STREET: 707 WESTCHESTER AVENUE

CITY: WHITE PLAINS

STATE: NEW YORK

COUNTRY: USA

ZIP: 10604

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/963, 290A

FILING DATE: 25-OCT-1989

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8923998

NAME: HARACZ, Stephen M  
 REGISTRATION NUMBER: 33,397  
 REFERENCE/DOCKET NUMBER: NO 2739/39/01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 914 328-0055  
 FAX: 914 328-0060  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "View of the 180bp TaqI-SPHI fragment from plasmid ECI carrying a part of the ENA3 gene"  
 FEATURE:  
 NAME/KEY: -  
 LOCATION: 9..11  
 OTHER INFORMATION: /note= "TaqI restriction site used to digest plasmid ECI. The Sphi restriction site is not sh  
 ; US-07-963-290A-5  
 Query Match 50.8%; Score 12.2; DB 1; Length 23;  
 Best Local Similarity 82.4%; Pred. No. 1.3e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 8 aggtcgtaatgatc 24  
 Db 1 ATGCCTGTAATGCAATTC 17